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(54) Title: POLYPEPTIDES FOR IDENTIFYING NEW HERBICIDALLY ACTIVE COMPOUNDS

(57) Abstract: The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding herbicides, to the use of the polypeptides identified for identifying new, herbicidally active compounds, and methods of finding modulators of these polypeptides. Likewise, the invention relates to the use of the polypeptides in assay methods for identifying herbicidally active compounds.

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Polypeptides for identifying new herbicidally active compounds

The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding herbicides, to the use of the polypeptides which have been identified for identifying new herbicidally active compounds, and to methods of finding modulators of this polypeptide. Equally, the invention relates to the use of the plant polypeptides in assay methods for identifying herbicidally active compounds.

Herbicides have great importance in agriculture to avoid undesired plant growth by using herbicides. In modern agriculture, the use of herbicides constitutes an imperative factor for safeguarding yields and profits. This is where herbicides must meet increasingly high demands with regard to their efficacy, costs and above all their ecofriendliness. There is therefore a constant demand for new substances, known as lead structures, which can be developed into even more potent and even more ecofriendly new herbicides.

To date, only a few molecular sites of action, known as targets, play a key role for the action of herbicidal compounds. Three quarters of the entire herbicide market are dominated by just 5 targets, which are the sites of action of these herbicides: acetolactate synthase, elongases for very long-chain fatty acids, enolpyruvylshikimate-3-phosphate synthase, the photosystem-II and the auxin signal cascade. The remaining quarter of the market comprises just 6 further important targets: acetal-coenzyme A carboxylase, glutamine synthase, photosystem I, phytoene desaturase, protoporphyrinogen oxidase and tubulin. Herbicides for all of these targets have been known for over 20 years. During this period, herbicides with other, new targets have not gained market relevance. This situation leads to a thorough knowledge and exploitation of these targets in the search for new herbicidally active lead structures. At the same time, however, the use of new targets is extremely important for an innovation in the search for new lead structures for the development of novel and superior herbicides.

To date it is generally customary to search for new lead structures in greenhouse tests. However, such tests require a good deal of labour and are expensive. The number of the substances, which can be tested in the greenhouse, is accordingly limited. However, even after suitable automation for increasing the throughput, 5 greenhouse screening does not allow any findings as to whether substances may be directed against a new target. This must be determined in very complex subsequent experiments.

An alternative to the search for lead structures which is nowadays generally customary is what is known as high-throughput screening or ultra-high-throughput screening (HTS or UHTS). This method, which was first established in pharmaceutical research, makes possible the automation of in-vitro assays for the search for lead structures for given targets. At the same time, it has been made possible to provide a high number of test substances by methods such as, for example, combinatorial chemistry. Thus, a multiplicity of methods has been developed as to how specific targets can be assayed by (U)HTS. The target-based search for lead structures for agricultural applications with the aid of (U)HTS does not differ from that for pharmaceutical applications and is therefore firmly 10 established at present.

(U)HTS makes it possible to test the action of several hundreds of thousands of substances on a specific target within a few days. However, existing experience in industry shows that it is not possible to find a lead structure for each new target, at 15 least not at present. It is therefore necessary to test a multiplicity of targets in order to identify suitable targets in addition to new herbicidal substances.

All of the five abovementioned herbicide targets which dominate the market, and most of the remaining targets, are only found in plants but not in animals. This is no coincidence but is due to the advantageous properties of such active compounds. 20 Thus, there is only little danger of a toxic effect on humans and the environment in

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plant-specific targets. This can be proved by comparing the two targets acetolactate synthase and protoporphyrinogen oxidase. At the beginning of the 80s, highly effective and innovative compounds were discovered for both targets, initially without knowing the target. A series of herbicides were quick to reach the market in
5 the case of the plant-specific target acetolactate synthase, so that acetolactate synthase is currently ranked third among the herbicide targets. Even though a very large variety of herbicides which act on protoporphyrinogen oxidase, which is also found in animals, is now known, the unfavourable toxicology of these products has as yet not led to an important commercial product.

10

Toxicological studies are complicated and expensive. As a rule, these studies are only performed when a certain basic development of new lead structures has already taken place. Even so, the research expenses up to this point are quite considerable. It is therefore advantageous to minimize the toxic effect of new herbicides, which is due
15 to the target, right at the beginning. This can be achieved by simply using those targets for the search for lead structures which are found only in plants, but not in animals.

20

Especially advantageous targets for new herbicides are searched for in essential biosynthetic pathways. Thus, for example, the biosynthesis of isoprenoids, building blocks of carotenoids and of plastoquinone and chlorophyll, are imperative for the growth of plants. The inhibition of a step in this plant-specific biosynthetic pathway, also known as the 1-desoxyxylulose-5-phosphate pathway, leads to the death of a plant (DE 199 35 967). The knowledge of the plant specificity of specific metabolic
25 pathways is currently fundamental knowledge in plant biochemistry (see, for example, B. B. Buchanan, W. Gruissem and R. L. Jones (Editors); "Biochemistry & Molecular Biology of Plants", American Society of Plant Physiologists, Rockville, MD, USA; 2000), even when it remains partially unclear which role certain proteins take on in the plant, and whether corresponding proteins or those with an equivalent
30 task are also found in, for example, mammals.

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Each new candidate herbicide must meet a number of criteria before it can be approved, and the choice of a suitable target is the first step in this search.

It is helpful to consider the existing genome information which is now available to the public, and to take note of some key criteria of herbicidal active compounds:

- 5 1. An active compound should be sufficiently selective and produce a herbicide which should be specific, or at least very selective, for plants (with regard to humans or animals).
- 10 2. An active compound should attack proteins or else genes which are imperative for the growth or the viability of the undesired plants, and
- 15 3. something should be known about the function of the target protein or target gene so that an assay and high-throughput screens can be established.

It is furthermore important for choosing suitable targets that the probability of identifying a new lead structure is considerably higher when the target has a natural binding property for ligands of low molecular weight. This is in contrast to, for example, individual protein components of large complexes with many subunits. The interference of protein-protein interactions by small ligands is less possible and requires, in principle, larger active compounds whose production costs are then frequently higher, so that a meaningful use of these active compounds as herbicides is made substantially more difficult. Targets with small natural ligands are, for example, enzymes, receptors and channels. Moreover, enzymes, receptors and channels can frequently be assayed more easily in assay methods (HTS or UHTS) than other proteins.

30 A possibility of recognizing plant-specific new targets is to test the enzymes or receptors and channels involved in plant-specific metabolic pathways or signal chains one after the other, using present-day biochemical knowledge (B. B. Buchanan, W.

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Gruissem and R. L. Jones (Editors); "Biochemistry & Molecular Biology of Plants", American Society of Plant Physiologists, Rockville, MD, USA; 2000). However, this route carries the risk of overlooking important properties of the proteins.

- 5 While new routes for, for example, based on sequence information in the field of antibiotic research have already been described (see, for example, Molly B. Schmid, Novel approaches to the discovery of antimicrobial agents, Curr. Opin. Chemical Biol., 2, 529-534, 1998.), a method of identifying suitable targets for the search for herbicides on the basis of existing data from sequencing work is as yet not available.
- 10 It was therefore the object of the present invention to describe a method which is suitable for identifying, in an efficient and reliable fashion, those nucleic acids or polypeptides encoded by them from among sequence information available in public databases, which can be used for the search for new herbicidal active compounds as plant-specific sites of action which can be obtained by a screening method. The object of the present invention was also to identify and to describe suitable target proteins by means of the method described and to make these available for use in screening methods for the search for new active compounds.
- 15
- 20 The complete knowledge of the genome of *Arabidopsis*, of humans and of many other organisms now allows to filter out, by means of computer-aided comparison of the proteins encoded in the genome, those proteins which occur in one organism but not another. Thus, it is also possible to recognize plant-specific proteins whose function was hitherto unelucidated.
- 25 In the present context, the term "plant-specific" is understood as meaning that no similarity with proteins from animals, in particular higher animals (Metazoa; in particular Chordata) is found.
- 30 A series of these plant-specific proteins, however, are also found in micro-organisms (for example bacteria, fungi).

In the present invention there is now described a possibility of identifying, from publicly available information and with the aid of computer-aided methods, those proteins and the nucleic acids encoding them which are suitable for use in methods 5 for identifying new herbicidally active compounds.

The comparison of the proteins encoded in various genomes is possible by means of a systematic alignment comparison (for example BLAST (Altschul et al., 1990), FastA (Lipman and Pearson, 1985, Pearson 1991), Search (Smith and Waterman, 10 Hmmer (Durbin et al., 1998)) between all proteins of one organism and those of the other organism. Preferably, one organism is selected, and the presence of the homologous sequence in other organisms is then studied.

In the present invention, all of the proteins encoded in the genome of *Arabidopsis thaliana* (hereinbelow abbreviated to "Arabidopsis") are compared with all of the other sequences which are accessible in public databases. The following databases 15 were used as source for the Arabidopsis polypeptides in the present invention:

- a) TAIR (Huala et al., 2001), which is a searchable relational database comprising information related to *Arabidopsis thaliana*, and
- b) GenBank (Benson et al., 2000), which is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences, including 20 protein translations.

25 Databases which can be used for the comparison are, for example, the following:

- a) SwissProt, which is a curated protein sequence database and provides a high level of annotations (e.g. function, domains structure, variants etc.)
- b) TrEMBL and TrEMBL-New (non-redundant protein databases), which are 30 computer-annotated supplements of Swiss Prot and contain all the translations of EMBL nucleotide sequence entries not yet integrated in SwissProt and

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whereby TrEMBL-New is a weekly update to TrEMBL which contains the protein-coding sequences from EMBLNEW

(see Bairoch and Apweiler, 2000).

5

All of the protein-encoding genes, and/or the polypeptides encoded by them, of the databases are compared with each other (pair-wise comparison; each polypeptide with each polypeptide) in order to find homologous similarities. The rigorous Smith-Waterman algorithm is used for this purpose.

10

To assess whether a given alignment constitutes evidence for homology, it helps to know how strong an alignment can be expected from chance alone. A local alignment without gaps consists simply of a pair of equal length segments, one from each of the two sequences being compared. A modification of the Smith-Waterman or Sellers 15 algorithms will find all segment pairs whose "scores" can not be improved by extension or trimming. These are called high-scoring segment pairs (HSPs). To analyze how high a score is likely to arise by chance, a model of random sequences is needed. For proteins, the simplest model chooses the amino acid residues in a sequence independently, with specific background probabilities for the various 20 residues. In the limit of sufficiently large sequence lengths m and n, the statistics of HSP scores are characterized by two parameters, K and lambda. Most simply, the expected number of HSPs with score at least S is given by the formula.

$$E = Kmne^{-\lambda S}$$

25

which is the so called E-value for the score S. The parameters K and lambda can be thought of simply as natural scales for the search space size and the scoring system respectively.

30

The measure for the similarity which is obtained is therefore an E-value (expect-value). As shown above, the E-value indicates the probability of which the existing

agreement between two proteins or else genes or nucleic acids is due to pure random chance. The smaller the E-value, the more significant a hit in the search. If, for example, the E-values are in the range of 1e-70, this means that owing to the size of the database, only 10^{-70} hits would have been expected with the search sequence.

5 This also means that the results are highly significant. In the case of two identical sequences, the E-value thus progresses towards zero. In the case of two entirely unrelated sequences, the E-value converges to values greater than one.

In the present method according to the invention, the criterion chosen for plant specificity and thus the suitability of the polypeptide according to the present invention, the E-value was chosen such that the exponent of the E-value of a paralogous or orthologous plant amino acid sequence must exceed that of a corresponding paralogous or orthologous animal or human sequence, in as far as such an animal or human sequence exists, at least by a factor of 3. The E-value of 10^{-30} is particularly suitable as limit for defining plant specificity. If the abovementioned factor decreases, it can be assumed with high probability that the homology between the plant sequence and the animal or human sequence is too high to classify a plant polypeptide as plant-specific and suitable for the use according to the invention in methods of finding herbicides.

20 The term "identity" as used in the present context refers to the number of sequence positions, which are identical in an alignment. In most cases, it is indicated as a percentage of the alignment length.

25 The term "similarity" as used in the present context, in contrast, requires the definition of a similarity matrix, that is to say a measure for the degree of similarity one wishes to assume between, for example, a valine and a threonine or a leucine.

30 The term "homology" as used in the present context, in turn, refers to evolutionary relationship. Two homologous proteins have developed from a joint precursor sequence. The term does not necessarily imply identity or similarity, apart from the

fact that homologous sequences are usually more similar (or have more identical positions in an alignment) than non-homologous sequences.

5 The term "orthologues" or "orthologous" as used in the present contexts refers to a functional counterpart, for example a protein in another organism, both having developed from a shared precursor. Normally, orthologues retain a shared function. In contrast, "paralogues" are genes or proteins resulting therefrom which have originated by duplication within a genome and which have assumed different functions during evolution which may still have similarity with each other.

10

Proteins are termed orthologous when

1. they have the highest level of pair-wise similarity (compared with the identities of the two proteins with all the other proteins in other genomes) and
- 15 2. the similarity is significant ($E < 0.01$).

20 The proteins encoded in the *Arabidopsis* genome and the results of the comparison with all the other public sequences were stored in a relational database (Oracle) in the present invention.

25 Such a relational database model was presented in 1970 by Codd et al. All of the data to be processed are shown in Tables (relatins) with a fixed number of columns and any desired number of lines (tupels). Data redundancies are avoided by distributing the information to individual tables. To date, this model remains the basis of most of the commercial database systems.

30 In general, the assigning of a description which is firstly correct and can secondly be searched for readily, what is known as an annotation, to each sequence constitutes a major problem in practice. An "annotation" of a sequence is the assigning of biologically relevant properties to this sequence of parts thereof.

By comparison of, possibly competing, alternative annotations in public databases and by individual corrections, a standardized annotation for each database entry has now been generated in the present invention. For example, the annotation takes such 5 a form that the description of enzymes, receptors and channels (transporters) starts with the respective functional name, that is, for example, with "acetolactate synthase".

An annotation was assigned to the sequence in a multi-step process; first, the 10 information content of words or terms within a sequence description were analysed and these words/terms were correspond categorized. Thus, the description "acetolactate synthase" leads to more information on a sequence than the descriptions "Unknown Protein" or "Hypothetical Protein" or "exon predicted by xgrail, quality marginal_shadowexon". This procedure first gives two categories of words/terms and, based on these categories, eventually two categories or sequence descriptions: 15 those with a low information content and those with a high information content.

Only the sequence descriptions with a high information content are used for 20 assigning an annotation to a sequence. These annotations obtained in this way are subsequently aligned in a suitable fashion with the annotations obtainable from TAIR. In the present invention, the TAIR annotation for a given sequence was adopted if such an annotation did exist.

This process was automated by developing suitable programs.
25 In a final step, the present annotations were rechecked and, if appropriate, corrected, to arrive at the final standardized annotation.

The database established within the present invention contains sequences from 30 Arabidopsis and the relevant descriptions(annotations) and E values in question and thus makes possible an efficient and meaningful analysis of the sequence data, which

results in the reliable identification of suitable plant-specific targets for the purposes of the present invention.

All the enzymes, receptors and channels or transporters with the above-described plant-specific E-values were then filtered out from the annotations of the database according to the invention with the aid of a suitable algorithm with suitable search terms. The polypeptides found by this method are shown in Table 1. In addition to the annotation of the polypeptide whose sequence is available by means of the reference to the sequence listing in the present application, Table 1 also shows which particular class of polypeptides it belongs to. Enzymes were arranged for example by classes such as "dehydrogenase" or "oxygenase". Receptors were searched for with the search term "receptor", but not "receptor kinase". Channels were searched for with the search term "channel" or "transporter". The table also contains what is known as the accession number of the sequence, in as far as it is known. The accession number provides information on the database or the number in which, or under which, the polypeptide sequence in question can be found. Furthermore, the table contains references to known homologous sequences from other organisms and a reference to the SEQ ID NO. under which the sequence in question is filed in the sequence listing.

20

Table 1:

ENTRY ID NO.	SEQ ID NO.	DESCRIPTION	CLASS
5	1	INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO SOLUBLE INORGANIC PYROPHOSPHATASE GB: AAD46520 GI:5669924 FROM [POPULUS TREMULA X POPULUS TREMULOIDES]	Phosphatase
12	2	FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 IDENTICAL TO GB: AAC99312 GI:4091810 FROM [ARABIDOPSIS THALIANA]	Synthase
33	3	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL GB:CAB40128 GI:4581201 FROM [ARABIDOPSIS THALIANA]	Channel
38	4	FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q40287 FROM [MANIHOT ESCULENTA]	Transferases
41	5	FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q40287 FROM [MANIHOT ESCULENTA]	Transferases
46	6	1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE(ATPIP5K1) GI:3702691 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	5-Kinase
50	7	DEHYDROGENASE GI:1922246 FROM [ARABIDOPSIS THALIANA] UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Dehydrogenases
53	8	SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GI:7248457 FROM [LOPHOPYRUM ELONGATUM]	Kinase, Protein
57	9	FERRIC REDUCTASE LIKE TRANSMEMBRANE COMPONENT	Reductase
58	10	FERRIC REDUCTASE LIKE TRANSMEMBRANE COMPONENT	Reductase

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72	11	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 GI:2852447 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
77	12	K EFFLUX ANTIPORTER KEAI IDENTICAL TO GB:AAD01191 GI:4101473 FROM [ARABIDOPSIS THALIANA]	Transporter
83	13	DIMETHYLADENOSE TRANSFERASE, PUTATIVE, 5' PARTIAL SIMILAR TO DIMETHYLADENOSE TRANSFERASE GB: AAC09322 GI:3005590 FROM [ARABIDOPSIS THALIANA]	Transferases
85	14	CUCUMISIN-LIKE SERINE PROTEASE GB: AAC18851 GI:317687 FROM [ARABIDOPSIS THALIANA]4[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Protease
87	15	RIBULOSE-1,5 BISPHOSPHATE CARBOXYLASE GB:L34291 GI:508550 FROM [PISUM SATIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Carboxylase
93	16	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45849 GI:5262223 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Oxidase
95	17	NUCLEOTIDE SUGAR EPIMERASE, PUTATIVE SIMILAR TO NUCLEOTIDE SUGAR EPIMERASE GB: AAC18831 GI:3093975 FROM [VIBRIO VULNIFICUS]	Epimerase
100	18	CHALCONE SYNTHASE HOMOLOG, GP U90341 2507617 AND ANOTHER SPECIFIC PROTEIN, GP Y14507 2326772	Synthase
118	19	SER-THR PROTEIN KINASE-LIKE PROTEIN GI:9294588 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Kinase, Protein
127	20	(1-4)-BETA-MANNAN ENDOHYDROLASE PRECURSOR, PUTATIVE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE PRECURSOR GI:9836826 FROM [LYCOPERSICON ESCULENTUM]	Hydrolase
132	21	CHITINASE, PUTATIVE SIMILAR TO CHITINASE GI:1237025 FROM [ARACHIS HYPOGAEA]	Chitinase
136	22	DIOXYGENASE, PUTATIVE SIMILAR TO DIOXYGENASE GI:1666096 FROM [MARAH MACROCARPUS]	Oxygenases

142	23	POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO POLYGALACTURONASE PG1 GB:AAD46483 GI:5669846 FROM [GLYCINE MAX].	Glycosylase
154	24	ALDEHYDE OXIDASE, PUTATIVE SIMILAR TO ALDEHYDE OXIDASE GB:BAA28630 GI:3172044 FROM [ARABIDOPSIS THALIANA]	
157	25	NUCLEOSIDE TRANSPORTER GB:AAF26446 GI:6715514 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transporter
158	26	BETA-XYLOSIDASE, PUTATIVE SIMILAR TO BETA-XYLOSIDASE GB:Z84377 GI:2102655 FROM [ASPERGILLUS NIGER]	Glycosylase
166	27	GLYCOSYL TRANSFERASE GB:CAB80706 GI:7268597 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transferases
167	28	CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB: AAC39336 GI:2827143 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase
172	29	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS]	Glycosylase
174	30	PECTINESTERASE, PUTATIVE SIMILAR TO PECTIN ESTERASE GI:1213628 FROM [PRUNUS PERSICA]	Esterase
185	31	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS]	Transferases
186	32	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS]	Transferases
187	33	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:860955 FROM [HYOSCYAMUS MUTICUS]	Transferases
188	34	GLUTATHIONE-S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE-S-TRANSFERASE GI:169887 FROM [SILENE VULGARIS]	Transferases

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197	35	LIPOAMIDE DEHYDROGENASE COMPONENT OF THE PYRUVATE DEHYDROGENASE COMPLEX E3, CONTAINS PF 00010 HELIX-LOOP-HELIX DNA-BINDING DOMAIN. ESTS GB T45640 AND GB T22783 COME FROM THIS GENE[PUTATIVE]	Dehydrogenases
209	36	FRUCTOKINASE, PUTATIVE PREDICTED BY GENEFINDER	Kinase
224	37	ISOAMYLASE SIMILAR TO GI 1652733 GLYCOGEN OPERON PROTEIN GLGX FROM SYNECHOCYSTIS SP. GENOME GB D90908. ESTS GB H36690, GB AA712462, GB AA651230 AND GB N95932 COME FROM THIS GENE[PUTATIVE]	Glycosylase
232	38	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE[HYPOTHETICAL PROTEIN SIMILAR TO]	N-Transferases
233	39	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ESTS EMB Z34690, GB T04168, GB H37738, GB T76913, GB T43801, AMD GB T21964[PUTATIVE]	Oxidase
234	40	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ESTS EMB Z34690, GB T04168, GB H37738, GB T76913, GB T43801, AMD GB T21964[PUTATIVE]	Oxidase
243	41	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428[HYPOTHETICAL PROTEIN SIMILAR TO]	Transferases
250	42	PROTEIN PHOSPHATASE SIMILAR TO GB:AAB97706[PUTATIVE]	Phosphatase
254	43	PROTOCHLOROPHYLLIDE REDUCTASE SIMILAR TO PROTOCHLOROPHYLLIDE REDUCTASE PRECUSOR; SIMILAR TO ESTS GB R30630, GB T46162, EMB Z26728, GB AA042736, AND GB AA042730[PUTATIVE]	Reductase
284	44	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASES[HYPOTHETICAL NEARLY IDENTICAL TO], ARABIDOPSIS PROTEIN F21B7.22, SIMILAR TO	Transferases
294	45	ACID PHOSPHATASE; LOCATION OF ESTS 110C2T7, GB T42036, AND 110C2XP, GB AI100245; SIMILAR TO	Phosphatase

297	46	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT HYPOTHETICAL GB Z98597 FROM S. POMBE. ESTS GB T45575 AND GB Z26435 AND GB AA394576 COME FROM THIS GENE	Receptor
301	47	SUBTILISIN PROTEASE STRONG SIMILARITY TO PROTEIN SBT1 GB X98929 FROM LYCOPERSICUM ESCULENTUM[PUTATIVE]	Protease
302	48	ABC TRANSPORTER, MULTI-DRUG RESISTANCE PROTEIN STRONG SIMILARITY TO MRP-LIKE ABC TRANSPORTER GB U92650 FROM A. THALIANA AND CANALICULAR MULTI-DRUG RESISTANCE PROTEIN GB L49379 FROM RATTUS NORVEGICUS	Transporter
303	49	SERINE/THREONINE PROTEIN PHOSPHATASE GB X83099 FROM S. CEREVISIAE[HYPOTHETICAL] PROTEIN CONTAINS SIMILARITY TO	Phosphatase
305	50	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE [PUTATIVE]	Transferases
308	51	DIMETHYLANILINE MONOOXYGENASE [PUTATIVE]	Oxygenases
311	52	ADENYLATE CYCLASE GB AF012921 FROM MAGNAPORTHE GRISAE. EST GB Z24512 COMES FROM THIS GENE; UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Cyclase
312	53	BETA-KETOACYL-COA SYNTHASE STRONG SIMILARITY TO BETA-KETO-COA SYNTHASE GB U37088 FROM SIMMONDSIA CHINENSIS[PUTATIVE]	Synthase
321	54	ETHYLENE RECEPTOR (ERS2). EST GB W43451. COMES FROM THIS GENE[PUTATIVE]	Receptor
324	55	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE SIMILAR TO ARABIDOPSIS 2A6 (GB X83096). EST GB T76913 COMES FROM THIS GENE[PUTATIVE]	Oxidase
327	56	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE STRONG SIMILARITY TO ARABIDOPSIS 2A6 (GB X83096)[PUTATIVE]	Oxidase
331	57	ALDO-KETO REDUCTASE BABESIA (GB M93122[HYPOTHETICAL PROTEIN SIMILAR TO]	Reductase

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350	58	DIMETHYLANILINE MONOOXYGENASE SIMILAR TO GB: AAC04900[PUTATIVE]	Oxygenases
357	59	PECTATE LYASE AII SIMILAR TO GB: CAB36835[PUTATIVE]	Lyase
380	60	SUCROSE-PHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GB: Y11795 FROM [CRATEROSTIGMA PLANTAGINEUM]	Synthase
390	61	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE IDENTICAL TO 1-AMINOCYCLOPROPANE-1- CARBOXYLATE OXIDASE (ACC OXIDASE) GB X66719 (EAT1). ESTS GB T43073, GB T5714, GB R90435, GB R44023, GB AA597926, GB AI099676, GB AA650810 AND GB 29725 COME FROM THIS GENE	Oxidase
403	62	O-GLCNAC TRANSFERASE SIMILAR TO RATTUS O- GLCNAC TRANSFERASE (GB U76557)[PUTATIVE]	Transferases
412	63	PEROXIDASE ATP12A STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATP11A (GB X98802)[PUTATIVE]	Oxidase
413	64	PEROXIDASE ATP12A STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATP11A (GB X98802)[PUTATIVE]	Oxidase
414	65	PEROXIDASE STRONG SIMILARITY TO ARABIDOPSIS PEROXIDASE ATPOX7A (GB X98321)[PUTATIVE]	Oxidase
418	66	ZINC TRANSPORTER SIMILAR TO ARABIDOPSIS FE(II) TRANSPORT PROTEIN (GB U27590)[PUTATIVE]	Transporter
419	67	PECTIN METHYLESTERASE SIMILAR TO PRUNUS PECTINESTERASE (GB X95991)[PUTATIVE]	Esterase
440	68	UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE GI:2149127 FROM [ARABIDOPSIS THALIANA]	Transferases
443	69	UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE GI:2149127 FROM [ARABIDOPSIS THALIANA]	Transferases

444	70	GLUCAN SYNTHASE HIGHLY SIMILAR TO PUTATIVE GLUCAN SYNTHASE GB:AAD15408[PUTATIVE]	Synthase
445	71	NA/H ANTIPORTER PROTEINS; N-TERMINAL HALF OF PROTEIN IS SIMILAR TO NA/H ANTIPORTER PROTEINS[HYPOTHETICAL PROTEIN SIMILAR TO]	Transporter
452	72	POLYGALACTURONASE SIMILAR TO GB: AAC23398[PUTATIVE]	Glycosylase
453	73	POLYGALACTURONASE SIMILAR TO GB: AAC23398[PUTATIVE]	Glycosylase
454	74	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE GB:AAD32293[PUTATIVE]	Transferases
455	75	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE GB:AAD32293[PUTATIVE]	Transferases
466	76	NPK1-RELATED PROTEIN KINASE 2 PREDICTED BY GENEMARK.HMM[PUTATIVE]	Kinase, Protein
472	77	CHITINASE, CLASS I, PUTATIVE SIMILAR TO GB: AAF69774 FROM [ARABIDOPSIS BLEPHAROPHYLLA] (PROC. NATL. ACAD. SCI. U.S.A. 97 (10), 5322-5327 (2000))	Chitinase
486	78	UDPG GLUCOSYLTRANSFERASE GB: AAB62270 GI: 2232354 FROM [SOLANUM BERTHAULTII], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Transferases
488	79	FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB: U62329 GI: 1915973 FROM [LYCOPERSICON ESCULENTUM]	Kinase
489	80	FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB: U37838 GI: 1052972 FROM [BETA VULGARIS]	Kinase
494	81	DELTA 9 DESATURASE IDENTICAL TO DELTA 9 DESATURASE GB: BAA25180 GI: 2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases
495	82	DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB: BAA25180 GI: 2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases

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496	83	DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases
498	84	DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GB:BAA25180 GI:2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases
511	85	LIPASE-LIKE PROTEIN SIMILAR TO LIPASE GB:AAD01804 GI:4103627 FROM [DIANTHUS CARYOPHYLLUS]	Lipase
520	86	DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GI:2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases
521	87	DELTA 9 DESATURASE, PUTATIVE SIMILAR TO DELTA 9 DESATURASE GI:2970034 FROM [ARABIDOPSIS THALIANA]	Desaturases
532	88	GLUCAN SYNTHASE, PUTATIVE SIMILAR TO GLUCAN SYNTHASE GB:AAD11794 [FILOBASIDIELLA NEOFORMANS VAR. NEOFORMANS]	Synthase
544	89	IRON/ASCORBATE OXIDOREDUCTASE FAMILY	Reductase
546	90	IRON/ASCORBATE OXIDOREDUCTASE FAMILY	Reductase
547	91	IRON/ASCORBATE OXIDOREDUCTASE FAMILY	Reductase
552	92	PROTEIN KINASE, 5' PARTIAL CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
555	93	RIBOKINASE, SUGAR KINASE, PUTATIVE SIMILAR TO RIBOKINASE GB:AAD00536 GI:4099074 FROM [PYROBACULUM AEROPHILUM]	Kinase
562	94	LIPASE, PUTATIVE SIMILAR TO LIPASE GB:AAD01804 GI:4103627 FROM [DIANTHUS CARYOPHYLLUS]	Lipase
564	95	PHYTOENE DEHYDROGENASE RELATED ENZYME UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF02032	Dehydrogenase
566	96	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GB:BAA11869 GI:1389566 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein

568	97	PROCESSING PEPTIDASE, CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE, PUTATIVE SIMILAR TO CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE GB:CAA71502 GI:2769566 FROM [ARABIDOPSIS THALIANA]	Protease
576	98	NA+/H+ ANTIPORTER GI:2347190 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transporter
581	99	MITOCHONDRIAL CARRIER PROTEINS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transporter
596	100	ALTERNATIVE NADH-DEHYDROGENASE GI:3718005 FROM [YARROWIA LIPOLYTICA] UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Dehydrogenases
597	101	PROTEASE ATP-DEPENDENT [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Protease
602	102	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA]	Transferases
603	103	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA]	Transferases
604	104	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:453245 FROM [MANIHOT ESCULENTA]	Transferases
621	105	PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO GB:CAB90633 FROM [FAGUS SYLVATICA]	Phosphatase
622	106	TROPINONE REDUCTASE-I, PUTATIVE SIMILAR TO GB:L20473 FROM [DATURA STRAMONIUM] (PROC. NATL. ACAD. SCI. U.S.A. 90, 9591-9595 (1993))	Reductase
623	107	TROPINONE REDUCTASE-I, PUTATIVE SIMILAR TO GB:L20473 FROM [DATURA STRAMONIUM] (PROC. NATL. ACAD. SCI. U.S.A. 90, 9591-9595 (1993))	Reductase
633	108	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069, EUKARYOTIC PROTEIN KINASE DOMAIN (1 COPY)	Kinase, Protein

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634	109	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN (1 COPY)	Kinase, Protein
642	110	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO GB: AAC50043 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 37 (4), 587-596 (1998))	Kinase, Protein
649	111	FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE, PUTATIVE SIMILAR TO GB: AAC99312 FROM [ARABIDOPSIS THALIANA] (PLANT J. (1999) IN PRESS)	Synthase
653	112	PHOSPHORIBOSYLANTHRANILATE ISOMERASE IDENTICAL TO GB: AAB03498 FROM [ARABIDOPSIS THALIANA] (CELL 83 (5), 725-734 (1995))	Isomerase
661	113	PROTEIN KINASE, PUTATIVE (FRAGMENT) SIMILAR TO GB: BAA94509 FROM [POPULUS NIGRA]	Kinase, Protein
663	114	L-ASCORBATE PEROXIDASE IDENTICAL TO GB: CAA42168 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 18 (4), 691-701 (1992))	Oxidase
683	115	HIGH-AFFINITY NITRATE TRANSPORTER NRT2 IDENTICAL TO GB: CAB09794 FROM [ARABIDOPSIS THALIANA]	Transporter
684	116	HIGH-AFFINITY NITRATE TRANSPORTER ACH2 IDENTICAL TO GB: AAC35884 FROM [ARABIDOPSIS THALIANA] (PLANT J. 17 (5), 563-568 (1999))	Transporter
695	117	DTDP-GLUCOSE 4-6-DEHYDRATASE GI: 9759250 FROM [ARABIDOPSIS THALIANA] [UNKNOWN PROTEIN CONTAINS SIMILARITY TO]	Dehydratase
696	118	PROTEASE GI: 4415912 FROM [ARABIDOPSIS THALIANA] [HYPOTHETICAL PROTEIN SIMILAR TO] [PUTATIVE]	Protease
698	119	AMINO ACID PERMEASE GI: 7415521 FROM [ORYZA SATIVA] [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transporter
699	120	PREPHENATE DEHYDRATASE GI: 1008717 FROM [AMYCOLATOPSIS METHANOLICA] [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Dehydratase

702	121	ALPHA2,8-SIALYLTRANSFERASE GI:929684 FROM [MUS MUSCULUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transferases
724	122	ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE, Esterase PUTATIVE ALMOST IDENTICAL TO ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE GB:CAA85387 GI:634003 FROM [ARABIDOPSIS THALIANA]	Esterase
725	123	MG-CHELATASE, PUTATIVE SIMILAR TO MG-CHELATASE GB:AF014399 GI:2318116 FROM [PISUM SATIVUM]	Che latase
728	124	VIOLAXANTHIN DE-EPOXIDASE PRECURSOR (U44133) Oxidase SIMILAR TO EST GB N37612[PUTATIVE]	Oxidase
732	125	RECEPTOR KINASE, CLV1 SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE (POMOEA NIL) (U77888)[PUTATIVE]	Kinase, Protein
739	126	BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE Transf erases (PIR IJC5251), UNKNOWN PROTEIN SIMILAR TO	Transf erases
761	127	SUGAR TRANSPORT PROTEIN, ERD6 SIMILAR TO Transporter GB:BAA25989[PUTATIVE]	Transporter
769	128	AMIDASE (GB D16207). ESTS AMIDASE GB T20504,GB H36650,GB N97423,GB H36595 COME FROM THIS GENE; SIMILARITY TO	AMIDASE
772	129	BETA-MANNOSIDASE (GB U46067), UNKNOWN Glycosylase PROTEIN CONTAINS SIMILARITY TO BOS	Glycosylase
773	130	AMP-ACTIVATED PROTEIN KINASE Kinase, Protein (GB X95577)[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO] RATTUS	Kinase, Protein
785	131	PROTEIN PHOSPHATASE 2C SIMILAR TO Phosphatase GB: AAC16260[PUTATIVE]	Phosphatase
792	132	NICOTIANAMINE SYNTHASE SIMILAR TO Synthase GB:BAA74589[PUTATIVE]	Synthase
803	133	GALACTINOL SYNTHASE SIMILAR TO GB:AAD26116 Synthase FROM [BRASSICA NAPUS][PUTATIVE]	Synthase
807	134	LIPASE SIMILAR TO NODULINS AND LIPASE Lipase LOCATION OF EST E6C2T7 , GB AA042309. SIMILAR TO NODULINS GI 3328240, GI 2129854 AND OTHERS AND LIPASE, GI 2129636[PUTATIVE]	Lipase

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808	135	12-OXOPHYTODIENOATE REDUCTASE OPRI SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE, GI 2765083 AND OLD-YELLOW-ENZYME HOMOLOG, GI 2232254[PUTATIVE]	Reductase
812	136	SER/THR PROTEIN KINASE SIMILAR TO GB:AAD21713[PUTATIVE]	Kinase, Protein
814	137	BETA-1,3-GLUCANASE GB:AAD22663, LOCATION OF EST 192N12T7, GB R90355, UNKNOWN PROTEIN SIMILAR TO	Glycosylase
823	138	PECTINACETYLESTERASE PRECURSOR SIMILAR TO VIGNA RADIATA PECTINACETYLESTERASE PRECURSOR, GI 1431629[PUTATIVE]	Esterase
847	139	PHYTOCHELATIN SYNTHETASE SIMILAR TO GB:CAA07251[PUTATIVE]	Synthase
862	140	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR SIMILAR TO GB:P49294 AND TO A. THALIANA HEMA2 (GB U27118)[PUTATIVE]	Reductase
864	141	SUCROSE/H ⁺ SYMPORTER SIMILAR TO GB:CAA76367 AND VICIA SUCROSE TRANSPORT PROTEIN (GB Z93774)[PUTATIVE]	Transporter
865	142	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
868	143	REVERSE TRANSCRIPTASE SIMILAR TO GB:AAD29058[PUTATIVE]	Transcriptase
869	144	AMINO ACID PERMEASE GC SPLICE SITE AT POSITION 1256 IS PREDICTED FROM ALIGNMENT AND NOT CONFIRMED EXPERIMENTALLY. HIGHLY SIMILAR TO ARABIDOPSIS THALIANA AMINO ACID PERMEASE I GI 404019, AND OTHER AMINO ACID PERMEASES[PUTATIVE]	Transporter
873	145	XYLAN ENDOHYDROLASE SIMILAR TO GB:AAD27896 TO ENDOXYLANASES GI 1255238 (THERMOANAEROBACTERIUM THERMOSULFURIGENES), GI 1813595 (HORDEUM VULGARE) AND OTHERS[PUTATIVE]	Hydrolase
894	146	LECTIN RECEPTOR KINASE VERY SIMILAR TO GB:CAA69271[PUTATIVE]	Kinase, Protein

899	147	OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC PROTEIN (SP Q05016 YM71_YEAST [UNKNOWN PROTEIN SIMILAR TO DAUNORUBICIN C-13 (U77891); SIMILAR TO])	Reductase
904	148	GLUTATHIONE S-TRANSFERASE TSI-1 SIMILAR TO GLUTATHIONE S-TRANSFERASE (SP Q03666 GTX4_TOBAC); SIMILAR TO EST GB H36275[PUTATIVE]	Transferases
905	149	GLUTATHIONE S-TRANSFERASE TSI-1 SIMILAR TO GLUTATHIONE S-TRANSFERASE TSI-1 (GI 2190992); SIMILAR TO ESTS GB R29860, EMB Z29757, AND EMB Z29758[PUTATIVE]	Transferases
907	150	CELL RECEPTOR BETA CHAIN CDR3 (GI 3064031); SIMILAR TO NUCLEOPORIN NUP145 (SP P49687 N145_YEAST); SIMILAR TO ESTS GB N37877, EMB Z29159, AND EMB Z30865	Receptor
908	151	GLUCOSYL TRANSFERASE SIMILAR TO IMMEDIATE-EARLY SALICYLATE-INDUCED GLUCOSYLTTRANSFERASE (AC005167), PUTATIVE	Transferases
913	152	GERMIN-LIKE OXALATE OXIDASE SIMILAR TO ESTS GB T88481 AND GB AI099566	Oxidase
922	153	ENDOXYLOGLUCAN TRANSFERASE SIMILAR TO XYLOGLUCAN ENDOTRANSGLYCOSYLASE-RELATED PROTEIN XTR4 (PIR IS71223)[PUTATIVE]	Transferases
924	154	TYROSINE PHOSPHATASE 2 SIMILAR TO PROTEIN-TYROSINE PHOSPHATASE 2 (GI 3249071), SIMILAR TO EST GB N96456[PUTATIVE]	Phosphatase
929	155	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE 1 GI:7573596 FROM [POPULUS NIGRA]	Kinase, Protein
931	156	POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO POLYGALACTURONASE PG1 GI:5669846 FROM [GLYCINE MAX]	Glycosylase
937	157	PHOSPHORIBOSYL DIPHOSPHATE SYNTHASE STRONG SIMILARITY TO GI 4544471 F23E6.11 FROM ARABIDOPSIS THALIANA BAC GB AC006580[PUTATIVE]	Synthase

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941	158	LIPASE SIMILAR TO GB X02844 LIPASE PRECURSOR FROM STAPHYLOCOCCUS HYICUS. ESTS GB AI239406 AND GB T76725 COME FROM THIS GENE[PUTATIVE]	Lipase
943	159	PYRUVATE PHOSPHATE DIKINASE, PEP/PYRUVATE BINDING DOMAIN	Kinase
948	160	ALDO/KETO REDUCTASE FAMILY, AUXIN-INDUCED PROTEIN STRONG SIMILARITY TO GB X56267 AUXIN-INDUCED PROTEIN (PCNT115) FROM NICOTIANA TABACUM 00248[PUTATIVE]	Reductase
952	161	RECEPTOR KINASE, 3' PARTIAL IDENTICAL TO GB:AAB65490	Kinase, Protein
963	162	ZIP4, A PUTATIVE ZINC TRANSPORTER PER SUGGESTION BY DR. NATASHA M. GROTH (PNAS, VOL 95., 7220-7224)	Transporter
969	163	SER/THR PROTEIN KINASE ISOLOG	Kinase, Protein
973	164	LYSOPHOSPHOLIPASE ISOLOG	Lipase
977	165	LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE GB:AAC27895 GI:3360291 FROM [ZEA MAYS]	Kinase, Protein
981	166	SECRETORY CARRIER MEMBRANE PROTEIN, PUTATIVE SIMILAR TO SECRETORY CARRIER MEMBRANE PROTEIN GB:AAF36686 GI:7109228 FROM [ARABIDOPSIS THALIANA]	Transporter
982	167	BIFUNCTIONAL NUCLEASE BFNI ALMOST IDENTICAL TO BIFUNCTIONAL NUCLEASE BFNI GB:AAD00693 GI:4099831 FROM [ARABIDOPSIS THALIANA]	Nuclease
992	168	SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GB:Y12530 GI:2181187 FROM [BRASSICA OLERACEA]	Kinase, Protein
994	169	SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE KINASE GB:Y12531 GI:2181189 FROM [BRASSICA OLERACEA]	Kinase, Protein
997	170	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GB:AAC95353 GI:4008010 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein

998	171	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 GB:BAA23676 GI:2662048 FROM [BRASSICA RAPA]	Kinase, Protein
1001	172	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1279597 FROM [NICOTIANA PLUMBAGINIFOLIA]	Esterase
1005	173	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1783311 FROM [BRASSICA OLERACEA]	Kinase, Protein
1008	174	SERINE/THREONINE PROTEIN KINASE EMB CAA69216 CONTAINS SIMILARITY TO EXTENSIN PROTEIN GI:512380 FROM [BRASSICA NAPUS][SIMILAR TO]	Kinase, Protein
1019	175	ENDO-XYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO ENDO-XYLOGLUCAN TRANSFERASE GI:2244732 FROM [GOSSYPIUM HIRSUTUM]	Transferases
1022	176	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1617583 FROM [LYCOPERSICON ESCULENTUM]	Esterase
1023	177	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO FRUIT-SPECIFIC PECTIN METHYLESTERASE GI:1617583 FROM [LYCOPERSICON ESCULENTUM]	Esterase
1035	178	GLYCOGEN SYNTHASE STRONG SIMILARITY TO GB X95759 SOLUBLE-STARCH-SYNTHASE PRECURSOR (SSIII) FROM SOLANUM TUBEROSUM[PUTATIVE]	Synthase
1040	179	RETICULINE OXIDASE STRONG SIMILARITY TO GB AF049347. BERBERINE BRIDGE ENZYME FROM BERBERIS STOLONIFERA[PUTATIVE]	Oxidase
1042	180	PREPHENATE DEHYDRATASE CHLOROPLAST SIMILAR TO GI 2392772 AND IS A MEMBER OF THE PF 00800 PREPHENATE DEHYDRATASE FAMILY. ESTS GB T21562 AND GB T21062 COME FROM THIS GENE[PUTATIVE]	Dehydratase
1046	181	BETA-1,3-GLUCANASE SIMILAR TO GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE PRECURSOR GB Z28697 FROM NICOTIANA TABACUM. ESTS GB Z18185 AND GB AA605362 COME FROM THIS GENE[PUTATIVE]	Glycosylase

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1047	182	LACTOYLGLUTATHIONE LYASE-LIKE PROTEIN SIMILAR TO PROTEIN GB Z74962 FROM BRASSICA OLERACEA WHICH IS SIMILAR TO BACTERIAL YRN1 AND HEAHIO PROTEINS. ESTS GB T21954, GB T04283, GB Z37609, GB N37366, GB R90704, GB F15500 AND GB F14353 COME FROM THIS GENE	Lyase
1055	183	PECTATE LYASE-LIKE PROTEIN SIMILAR TO STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR GB X55193 AND PECTATE LYASE P59 PRECURSOR GB X15499 FROM LYCOPERSICON ESCULENTUM	Lyase
1063	184	PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE SIMILAR TO PYROPHOSPHATE-DEPENDENT PHOSPHOFUCTOKINASE BETA SUBUNIT GB Z32850 FROM RICINUS COMMUNIS. ESTS GB N65773, GB N64925 AND GB F15232 COME FROM THIS GENE[PUTATIVE]	1-Transferases
1064	185	1-AMINO-CYCLOPROPANE-CARBOXYLIC ACID OXIDASE (ACC OXIDASE) STRONG SIMILARITY TO AMINO-CYCLOPROPANE-CARBOXYLIC ACID OXIDASE GB L27664 FROM BRASSICA NAPUS. ESTS GB Z48548 AND GB Z48549 COME FROM THIS GENE[PUTATIVE]	Oxidase
1158	186	NITRATE TRANSPORTER, PUTATIVE SIMILAR TO GB:CAB09794 FROM [ARABIDOPSIS THALIANA]	Transporter
1163	187	BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE CONTAINS SIMILARITY TO GI 4417304 F15011.7 PUTATIVE BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE FROM ARABIDOPSIS THALIANA BAC GB AC006446[PUTATIVE]	Transferases
1170	188	CYTOCHROME P450 MONOOXYGENASE STRONG SIMILARITY TO GB D78605 CYTOCHROME P450 MONOOXYGENASE FROM ARABIDOPSIS THALIANA AND IS A MEMBER OF THE PF 00067 CYTOCHROME P450 FAMILY[PUTATIVE]	Oxygenases

1177	189	CYTOCHROME P450 MONOOXYGENASE STRONG SIMILARITY TO GI 3313615 F21J9.9 FROM ARABIDOPSIS THALIANA AND IS A MEMBER OF THE PF 00067 CYTOCHROME P450 FAMILY[PUTATIVE]	Oxygenases
1187	190	GLYCOSYL TRANSFERASE GI:6862930 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transferases
1190	191	ALLENE OXIDE CYCLASE, PUTATIVE SIMILAR TO ALLENE OXIDE CYCLASE GI:8977961 FROM [LYCOPERSICON ESCULENTUM]	Cyclase
1204	192	STEROID SULFOTRANSFERASE, PUTATIVE SIMILAR TO STEROID SULFOTRANSFERASE 1 GI:3420004 FROM [BRASSICA NAPUS]	Transferases
1220	193	NADPH-CYTOCHROME P450 REDUCTASE GI:10442765 FROM [TRITICUM AESTIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Reductase
1241	194	2-HYDROXY-6-OXO-7-METHYLOCTA-2,4-DIENOATE HYDROLASE GI:2822275 FROM [PSEUDOMONAS PUTIDA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Hydrolase
1242	195	BETA 1,3-GLUCANASE (GLC1) GI:924952 FROM [TRITICUM AESTIVUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Glycosylase
1260	196	RIBULOSE-1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT N-METHYLTRANSFERASE HIGHLY SIMILAR TO RIBULOSE-1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT N-METHYLTRANSFERASE, GI 1731475. RARE GC INTRON SPLICE SITE AT 49572 IS INFERRED FROM PROTEIN ALIGNMENT AND IS NOT CONFIRMED EXPERIMENTALLY[PUTATIVE]	Transferases
1263	197	XYLOGLUCAN FUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO XYLOGLUCAN FUCOSYLTRANSFERASE GI:5231145 FROM [ARABIDOPSIS THALIANA]	Transferases
1265	198	LIPOAAMIDE DEHYDROGENASE, PUTATIVE	Dehydrogenases

1268	199	2-OXOACID DEPENDENT DIOXYGENASE, DIOXYGENASE-LIKE PROTEIN VERY SIMILAR TO ADVENTITIOUS ROOTING RELATED OXYGENASE; VERY SIMILAR TO 2-OXOACID DEPENDENT DIOXYGENASE FROM MALUS DOMESTICA, GI 3492806	Oxygenases
1269	200	2-OXOACID DEPENDENT DIOXYGENASE, DIOXYGENASE-LIKE PROTEIN VERY SIMILAR TO ADVENTITIOUS ROOTING RELATED OXYGENASE; VERY SIMILAR TO 2-OXOACID DEPENDENT DIOXYGENASE FROM MALUS DOMESTICA, GI 3492806	Oxygenases
1274	201	MANDELONITRILE LYASE SIMILAR TO MANDELONITRILE LYASES GB:P52707, P52706, AND O50048; CONTAINS MC OXIDOREDUCTASES PROTEIN MOTIF[PUTATIVE]	Reductase
1275	202	MANDELONITRILE LYASE SIMILAR TO MANDELONITRILE LYASES GB:P52707, P52706, AND O50048; CONTAINS MC OXIDOREDUCTASES PROTEIN MOTIF[PUTATIVE]	Reductase
1277	203	RIBONUCLEASE CONTAINS RIBONUCLEASE T2 FAMILY HISTIDINE PROTEIN MOTIF[PUTATIVE]	Nuclease
1278	204	RIBONUCLEASE CONTAINS RIBONUCLEASE T2 FAMILY HISTIDINE PROTEIN MOTIF[PUTATIVE]	Nuclease
1281	205	NUCLEOSIDE TRIPHOSPHATASE, 3' PARTIAL SIMILAR TO GB: AAC32915[PUTATIVE]	Phosphatase
1284	206	ACID PHOSPHATASE, PUTATIVE SIMILAR TO ACID PHOSPHATASE GI:5360721 FROM [LUPINUS ALBUS]	Phosphatase
1294	207	RECEPTOR-LIKE PROTEIN KINASE GI:2947063 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Kinase, Protein
1297	208	PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GI:2463509 FROM [ZINNIA ELEGANS]	Lyase
1298	209	GLYOXAL OXIDASE GI:399594 FROM [PHANEROCHAETE CHRYSOSPORIUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Oxidase

1301	210	DNA POLYMERASE III GAMMA AND TAU SUBUNITS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Polymerase
1309	211	ANIONIC PEROXIDASE, PUTATIVE SIMILAR TO ANIONIC PEROXIDASE GI:170202 FROM [NICOTIANA SYLVESTRIS]	Oxidase
1310	212	ANIONIC PEROXIDASE, PUTATIVE SIMILAR TO ANIONIC PEROXIDASE GI:170202 FROM [NICOTIANA SYLVESTRIS]	Oxidase
1321	213	NA+/H+ ANTIPORTER, PUTATIVE SIMILAR TO NA+/H+ ANTIPORTER GB:CAA69925 GI:1655702 FROM [XENOPUS LAEVIS]	Transporter
1326	214	PURPLE ACID PHOSPHATASE, PUTATIVE CONTAINS PFAM PROFILE: PF02227 PURPLE ACID PHOSPHATASE	Phosphatase
1328	215	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDO-TRANSGLYCOSYLASE GB:CAA63553 GI:1769907 [ARABIDOPSIS THALIANA], IDENTICAL TO ENDOXYLOGLUCAN TRANSFERASE RELATED PROTEIN GB:BAA20290, GI:2154611 [ARABIDOPSIS THALIANA]	Transferases
1337	216	ASPARTATE-SEMALDEHYDE DEHYDROGENASE, PUTATIVE SIMILAR TO ASPARTATE-SEMALDEHYDE DEHYDROGENASE SP:O31219 [LEGIONELLA PNEUMOPHILA]	Dehydrogenases
1345	217	PECTINESTERASE GB:X85216 GI:732912 [PHASEOLUS VULGARIS]; UNKNOWN PROTEIN SIMILAR TO	Esterase
1361	218	GLUTAMINE AMIDOTRANSFERASE CLASS-IHISTONE ACETYLTRANSFERASE HAT B HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00117	Transferases
1362	219	GLYCEROL KINASE IDENTICAL TO SP:P34893 FROM [ARABIDOPSIS THALIANA] (J. MOL. BIOL. 251 (4), 533-549 (1995))[PUTATIVE]	Kinase
1370	220	FAD/NADH-BINDING DOMAIN. ESTS GB H76345 AND GB AA651465 COME FROM THIS GENE	Reductase
1389	221	CYSTATHIONINE BETA SYNTHASE DOMAIN [HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase

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1409	222	RECEPTOR LECTIN KINASE, PUTATIVE SIMILAR TO RECEPTOR LECTIN KINASE 3 GI:4100060 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
1410	223	OXIDOREDUCTASE GI:6751707 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Reductase
1411	224	GIBBERELLIN 3 BETA-HYDROXYLASE, PUTATIVE SIMILAR TO GIBBERELLIN 3 BETA-HYDROXYLASE GI:3982753 FROM [ARABIDOPSIS THALIANA]	Hydroxylase
1424	225	INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO INORGANIC PYROPHOSPHATASE GI:790478 FROM [NICOTIANA TABACUM]	Phosphatase
1450	226	CINNAMOYL COA REDUCTASE, PUTATIVE SIMILAR TO CINNAMOYL COA REDUCTASE GI:2058310 FROM [EUCALYPTUS GUNNII]	Reductase
1454	227	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN GI:4581207 FROM [ARABIDOPSIS THALIANA]	Channel
1464	228	WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1465	229	WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1466	230	WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1467	231	SERINE/THREONINE-SPECIFIC PROTEIN KINASE GI:7270012 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Kinase, Protein
1468	232	WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein

1469	233	WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1470	234	WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1475	235	PROTEIN PHOSPHATASE 2C SIMILAR TO GB: AAC36699[PUTATIVE]	Phosphatase
1479	236	WALL-ASSOCIATED KINASE SIMILAR TO GB AJ012423 WALL-ASSOCIATED KINASE 2 FROM ARABIDOPSIS THALIANA[PUTATIVE]	Kinase, Protein
1487	237	3-DEOXY-D-MANNO-2-OCTULOSONATE-8-PHOSPHATE SYNTHASE SIMILAR TO GB Y14272 3-DEOXY-D-MANNO-2-OCTULOSONATE-8-PHOSPHATE SYNTHASE FROM PISUM SATIVUM[PUTATIVE]	Synthase
1491	238	NA/H ANTIPORTER SIMILAR TO GI 4835769 T8K14.18 PUTATIVE NA/H ANTIPORTER ISOLOG FROM ARABIDOPSIS THALIANA BAC GB AC007202[PUTATIVE]	Transporter
1514	239	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
1525	240	INORGANIC PYROPHOSPHATASE, PUTATIVE SIMILAR TO VACUOLAR-TYPE H+-TRANSLOCATING INORGANIC PYROPHOSPHATASE GI:6901678 FROM [ARABIDOPSIS THALIANA]	Phosphatase
1529	241	H+-ATPASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO H+-ATPASE CATALYTIC SUBUNIT GI:6518112 FROM [CITRUS UNSHIU]	ATPase
1546	242	SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, 73% IDENTICAL TO SRG1 [ARABIDOPSIS THALIANA] (GI 479047). LOCATION OF ESTS 147E17T7 (GB T76176) AND 136D2T7 (GB T45959)	Oxidase

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1547	243	SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, SIMILAR TO SRG1 PROTEIN [ARABIDOPSIS THALIANA] (GI 629561). LOCATION OF EST F1AST7 (GB N96370)	Oxidase
1560	244	POLYGALACTURONASE AFTER FIRST 29 AMINO ACIDS, 43% IDENTICAL TO POLYGALACTURONASE [MEDICAGO SATIVA] (GI 3413322)[PUTATIVE]	Glycosylase
1561	245	RIBOKINASE [PUTATIVE]	Kinase
1562	246	GLUTATHIONE TRANSFERASE ONE OF THREE REPEATED PUTATIVE GLUTATHIONE TRANSFERASES. 72% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934)[PUTATIVE]	Transferases
1563	247	GLUTATHIONE TRANSFERASE SECOND OF THREE REPEATED PUTATIVE GLUTATHIONE TRANSFERASES. 72% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934). LOCATION OF ESTS 191A10T7 (GB R90188) AND 17IN13T7 (GB R65532)[PUTATIVE]	Transferases
1564	248	GLUTATHIONE TRANSFERASE ONE OF THREE REPEATED GLUTATHIONE TRANSFERASES. 65% IDENTICAL TO GLUTATHIONE TRANSFERASE [ARABIDOPSIS THALIANA] (GI 4006934). LOCATION OF EST 141CST7 (GB T46669)[PUTATIVE]	Transferases
1568	249	LEUCINE-RICH RECEPTOR PROTEIN KINASE 34% IDENTICAL TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE [IPOMOEA NIL] (GI 1684913) AND 35% IDENTICAL TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE [MALUS DOMESTICA] (GI 3641252)[PUTATIVE]	Kinase, Protein
1569	250	RECEPTOR PROTEIN KINASE APPROXIMATELY 30% IDENTICAL TO DISEASE RESISTANCE GENES [LYCOPERSICON PIMPINELLIFOLIUM] (GI 1184077 AND GI 1184075) AND [LYCOPERSICON ESCULENTUM] (GI 3894387 AND GI 3894393)[PUTATIVE]	Kinase, Protein

1570	251	RECEPTOR PROTEIN KINASE APPROXIMATELY 30% IDENTICAL TO DISEASE RESISTANCE PROTEINS [LYCOPERSICON ESCULENTUM] (GI 3894387 AND GI 3894393) AND [LYCOPERSICON PIMPINELLIFOLIUM] (GI 1184075 AND GI 1184077)[PUTATIVE]	Kinase, Protein
1584	252	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD22368 GI:4544460 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
1600	253	PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GI:3242077 FROM [ARABIDOPSIS THALIANA]	Phosphatase
1601	254	PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GI:3242077 FROM [ARABIDOPSIS THALIANA]	Phosphatase
1618	255	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE INRPK1 GI:1684913 FROM [IPOMOEA NIL]	Kinase, Protein
1634	256	WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
1642	257	12-OXOPHYTODIENOATE REDUCTASE, PUTATIVE SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE OPR1 GI:3882355 FROM [ARABIDOPSIS THALIANA]	Reductase
1644	258	12-OXOPHYTODIENOATE REDUCTASE, PUTATIVE SIMILAR TO 12-OXOPHYTODIENOATE REDUCTASE GI:4894182 FROM [LYCOPERSICON ESCULENTUM]	Reductase
1653	259	THREONYL-TRNA SYNTHETASES [HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	
1657	260	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP- TYPE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF00254	Isomerase
1669	261	BETA-GLUCAN-ELICITOR RECEPTOR, PUTATIVE SIMILAR TO BETA-GLUCAN-ELICITOR RECEPTOR GB:D78510 GI:1752733 FROM [GLYCINE MAX]	Receptor

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1674	262	LYSOPHOSPHOLIPASE HOMOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE HOMOLOG GB:AAB97366 GI:2801536 FROM [ORYZA SATIVA]	Lipase
1681	263	PEPTIDYL-TRNA HYDROLASE GB:D64003 GI:1001200 FROM [SYNECHOCYSTIS SP][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Hydrolase
1683	264	LIPASE GB:AAF36744 GI:7109480 FROM [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Lipase
1687	265	2-ISOPROPYLMALATE SYNTHASE, PUTATIVE SIMILAR TO 2-ISOPROPYLMALATE SYNTHASE GB:AF004165 GI:2213881 FROM [LYCOPERSICON PENNELLII]	Synthase
1695	266	GLYCOSYL TRANSFERASE FAMILY 8, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF01501	Transferases
1696	267	FLAVONOL 4'-SULFOTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 4'-SULFOTRANSFERASE GI:168168 FROM [FLAVERIA CHLORAEFOLIA]	Transferases
1702	268	BETA-1,3-GLUCANASE-LIKE PROTEIN GI:9758115 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO	Glycosylase
1705	269	REVERSE TRANSCRIPTASE DNA DEPENDENT GI:2920563 FROM [SPRAGUEA LOPHII], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Transcriptase
1706	270	ALPHA GALACTOSYLTTRANSFERASE, PUTATIVE SIMILAR TO ALPHA GALACTOSYLTTRANSFERASE GI:5702018 FROM [TRIGONELLA FOENUM-GRAECUM]	Transferases
1723	271	ISOCHORISMATE SYNTHASE, PUTATIVE SIMILAR TO ISOCHORISMATE SYNTHASE GI:3348077 FROM [ARABIDOPSIS THALIANA]	Synthase
1739	272	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4006833 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
1743	273	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase

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1745	274	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465925 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
1753	275	POLYGALACTURONASE-LIKE PROTEIN GI:10177371 FROM [ARABIDOPSIS THALIANA] [HYPOTHETICAL PROTEIN SIMILAR TO]	Glycosylase
1774	276	WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO GB:CAB42872 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 39 (6), 1189-1196 (1999))	Kinase, Protein
1788	277	2-HYDROXYISOFLAVONE REDUCTASE, PUTATIVE SIMILAR TO PIR:T08106 FROM [BETULA PENDULA]	Reductase
1789	278	GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GB:BAA90672 FROM [ORYZA SATIVA]	Reductase
1790	279	GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GB:BAA90672 FROM [ORYZA SATIVA]	Reductase
1793	280	RIBOKINASE, PUTATIVE SIMILAR TO GB:AAD00536 FROM [PYROBACULUM AEROPHILUM]	Kinase
1808	281	PROTEASE LA (LON) ATP-DEPENDENT DOMAIN	Protease
1812	282	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL PROTEIN, PUTATIVE SIMILAR TO CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL GI:4581207 FROM [ARABIDOPSIS THALIANA]	Channel
1836	283	FERREDOXIN-NADP REDUCTASE PRECURSOR, PUTATIVE SIMILAR TO GB:M25528 FROM [MESEMBRYANTHEMUM CRYSTALLINUM]	Reductase
1838	284	C-8,7 STEROL ISOMERASE IDENTICAL TO GB:AAD03489 FROM [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 38 (5), 807-815 (1998))	Isomerase
1848	285	SUBTILISIN PROTEASE	Protease
1849	286	SUBTILISIN PROTEASE	Protease

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1863	287	S-ADENOSYL-METHIONINE-STEROL-C-METHYLTRANSFERASE IDENTICAL TO STEROL-C-METHYLTRANSFERASE GI:1061040 FROM [ARABIDOPSIS THALIANA]	Transferases
1894	288	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:2852447 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
1911	289	SUGAR TRANSPORTER PROTEIN NEARLY IDENTICAL TO ARABIDOPSIS SUGAR TRANSPORTER, GI 1495273[PUTATIVE]	Transporter
1913	290	INORGANIC PHOSPHATE TRANSPORTER PROTEIN SIMILAR TO GB:CAA67395[PUTATIVE]	Transporter
1922	291	PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT SIMILAR TO GB:AAC67587 FROM [CITRUS X PARADISI] AND GB:Q41140 FROM [RICINUS COMMUNIS][PUTATIVE]	Kinase
1937	292	O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA]	Transferases
1938	293	O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA]	Transferases
1939	294	ATPASE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA][PUTATIVE]	ATPase
1940	295	O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF28353 FROM [FRAGARIA X ANANASSA]	Transferases
1959	296	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
1968	297	FLAVIN-CONTAINING MONOOXYGENASES, PUTATIVE IDENTICAL TO PUTATIVE FLAVIN-CONTAINING MONOOXYGENASES GB:AAF87896 GI:9454573 FROM [ARABIDOPSIS THALIANA]	Oxygenases
1969	298	CARBOXYVINYLCARBOXYPHOSPHONATE PHOSPHORYLMUTASE GB:O49290 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Mutase

1988	299	SECA-TYPE CHLOROPLAST PROTEIN TRANSPORT FACTOR SIMILAR TO GB X82404 CHLOROPLAST SECA PROTEIN FROM PISUM SATIVUM[PUTATIVE]	Transporter
2007	300	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM]	Esterase
2008	301	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM]	Esterase
2014	302	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, PUTATIVE SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE GB:CAB53377 GI:5777366 FROM [ARABIDOPSIS THALIANA]	Kinase
2044	303	TREHALOSE-6-PHOSPHATE PHOSPHATASE, PUTATIVE SIMILAR TO TREHALOSE-6-PHOSPHATE PHOSPHATASE GI:2944180 FROM [ARABIDOPSIS THALIANA]	Phosphatase
2051	304	PROTEIN PHOSPHATASE TYPE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE TYPE 2C GI:4336436 FROM [LOTUS JAPONICUS]	Phosphatase
2056	305	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA]	Transferases
2057	306	UDP-GLUCOSE GLUCOSYLTRANSFERASE IDENTICAL TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA]	Transferases
2058	307	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA]	Transferases
2059	308	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE, 5' PARTIAL SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA]	Transferases
2060	309	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:6561805 FROM [SORGHUM BICOLOR]	Transferases

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2079	310	PHOSPHORIBOSYLANTHANILATE TRANSFERASE, PUTATIVE SIMILAR TO PHOSPHORIBOSYLANTHANILATE TRANSFERASE GI:1396053 FROM [PISUM SATIVUM]	Transfases
2084	311	TRNA ADENYLYLTRANSFERASE SIMILAR TO TRNA ADENYLYLTRANSFERASE GB U15930 FROM LUPINUS ALBUS. EST GB AA721797 COMES FROM THIS GENE[PUTATIVE]	Transfases
2089	312	SUCROSE TRANSPORT PROTEIN, SUC2 STRONG SIMILARITY TO GB:S38196 SUCROSE TRANSPORT PROTEIN SUC2 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
2090	313	WALL-ASSOCIATED KINASE CONTAINS SIMILARITY TO SERINE/THREONINE KINASE GB Y12531 FROM BRASSICA OLERACEA[PUTATIVE]	Kinase, Protein
2111	314	PHOSPHOMETHYL PYRIMIDINE KINASE PROBABLE THIAMIN BIOSYNTHETIC ENZYME, LOCATION OF EST GB AA395737, GB T21651	Kinase
2119	315	NADPH OXIDASE FLAVOCYTOCHROME SUPEROXIDE- GENERATING HIGHLY SIMILAR TO GB:CAA70769, FRO1 AND GB:CAA70770, FRO2 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Oxidase
2125	316	AUXIN TRANSPORT PROTEIN STRONGLY SIMILAR TO AUXIN TRANSPORT PROTEIN GB:AAD52697[PUTATIVE]	Transporter
2137	317	PECTINESTERASE SIMILAR TO GB:AAB57669, LOCATION OF EST GB Z35063 AND GB Z35062[PUTATIVE]	Esterase
2154	318	2-HEXPRENYL-1,4-NAPHTHOQUINONE METHYLTRANSFERASE GB:BAA25267 GI:2982680 FROM [MICROCOCCUS LUTEUS]SERINE O- ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52 (PIR S71207) SPORE GERMINATION PROTEIN C2 SIMILAR TO	Transfases
2164	319	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GB:BAA88472 GI:6624205 FROM [CUCUMIS SATIVUS]	Glycosylase

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2165	320	POLYGALACTURONASE PRECURSOR [PUTATIVE]	Glycosylase
2166	321	GLUCOSYLTRANSFERASE GB:AAD15455 GI:4263795 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transferases
2187	322	CARBONIC ANHYDRASE [PUTATIVE]	Anhydrase
2212	323	REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO REVERSE TRANSCRIPTASE GB:BAA20419 GI:2193870 FROM [MUS MUSCULUS]	Transcriptase
2220	324	GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO BETA-(1-3)-GLUCOSYL TRANSFERASE GB: AAC62210 GI:3687658 FROM [BRADYRHIZOBIUM JAPONICUM]	Transferases
2222	325	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE SIMILAR TO GB:AAB64022[PUTATIVE]	Transferases
2223	326	PEROXIDASE SIMILAR TO PEROXIDASE ATP26A, GB:CAA72487[PUTATIVE]	Oxidase
2229	327	GLYCOSYL TRANSFERASE SIMILAR TO GB: AAC78704[PUTATIVE]	Transferases
2246	328	POLYKETIDE HYDROXYLASE FROM SEVERAL BACTERIAL SPECIES[HYPOTHETICAL PROTEIN SIMILAR TO]	Hydroxylase
2252	329	LYSINE/HISTIDINE-SPECIFIC PERMEASE SIMILAR TO GB: AAC49885, SIMILAR TO EST GB T13994[PUTATIVE]	Transporter
2253	330	DEACETYLVINDOLINE 4-O-ACETYLTRANSFERASE, GB: AAC9931; UNKNOWN PROTEIN SIMILAR TO	Transferases
2254	331	DEACETYLVINDOLINE 4-O-ACETYLTRANSFERASE, GB: AAC9931.1[HYPOTHETICAL PROTEIN SIMILAR TO]	Transferases
2256	332	RIBONUCLEASE III SIMILAR TO ESTS EMB Z18464 AND GB AA389811[PUTATIVE]	Nuclease
2271	333	PROTEIN KINASE SIMILAR TO GB:AAD21776, SIMILAR TO ESTS EMB Z18436, GB T21564, EMB F14127, AND GB T75836, DBJ D22341[PUTATIVE]	Kinase, Protein
2273	334	ANTHRANILATE SYNTHASE BETA SUBUNIT IDENTICAL TO ANTHRANILATE SYNTHASE BETA SUBUNIT GI:403434 FROM [ARABIDOPSIS THALIANA]	Synthase

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2277	335	ANTHRANILATE SYNTHASE BETA SUBUNIT IDENTICAL TO ANTHRANILATE SYNTHASE BETA SUBUNIT GI:403434 FROM [ARABIDOPSIS THALIANA]	Synthase
2278	336	PURPLE ACID PHOSPHATASE PRECURSOR GI:7331195 FROM [GLYCINE MAX][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Phosphatase
2294	337	WALL-ASSOCIATED KINASE, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 1 GI:3549626 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2296	338	TRNA ISOPENTENYL TRANSFERASE, PUTATIVE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GI:6006718 FROM [ARABIDOPSIS THALIANA]	Transferases
2301	339	DIHYDROFLAVONOL 4-REDUCTASE, PUTATIVE SIMILAR TO DIHYDROFLAVONOL 4-REDUCTASE GI:1332411 FROM [ROSA HYBRIDA]	Reductase
2308	340	LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA]	Transporter
2321	341	ESTERASE 6 GI:606998 FROM [DROSOPHILA SIMULANS], HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO	Esterase
2322	342	P-TYPE TRANSPORTING ATPASE, PUTATIVE SIMILAR TO P-TYPE TRANSPORTING ATPASE GI:9229867 FROM [ARABIDOPSIS THALIANA]	Transporter
2328	343	URIDINE KINASE GI:6899310 FROM [UREAPLASMA UREALYTICUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase
2345	344	ALPHA/BETA HYDROLASE GB:AAF67777 GI:7705098 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Hydrolase
2347	345	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Oxidase
2348	346	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Oxidase

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2349	347	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45849 GI:5262223 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Oxidase
2350	348	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA] UNKNOWN PROTEIN SIMILAR TO	Oxidase
2351	349	RETICULINE OXIDASE-LIKE PROTEIN GB:CAB45850 GI:5262224 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Oxidase
2352	350	FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE 1 SIMILAR TO PUTATIVE INTEGRAL MEMBRANE PROTEIN GB:AAD17424 GI:4335747 FROM [ARABIDOPSIS THALIANA]	Synthase
2353	351	BETA-1,3-GLUCANASE GB:AAD26909 GI:4662638 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Glycosylase
2389	352	RIBONUCLEASE 3 PRECURSOR IDENTICAL TO SP:P42815 FROM [ARABIDOPSIS THALIANA]	Nuclease
2393	353	REVERSE TRANSCRIPTASE GB:AAD17398[HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase
2402	354	REVERSE TRANSCRIPTASE GB:AAD22368[HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase
2409	355	NITRATE TRANSPORTER, PUTATIVE NITRATE TRANSPORTER NTL1 GB:AAC28086 GI:3377517 FROM [ARABIDOPSIS THALIANA]	Transporter
2417	356	GALACTOSYLTRANSFERASE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF01762	Transferases
2418	357	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB: AAF22517 GI:6652870 FROM [PAPAVER SOMNIFERUM]	Transferases
2419	358	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB: AAF22517 GI:6652870 FROM [PAPAVER SOMNIFERUM]	Transferases
2421	359	VALYL- TRNA SYNTHETASE, PUTATIVE SIMILAR TO VALYL-TRNA SYNTHETASE GB:P93736 GI:3122914 FROM [ARABIDOPSIS THALIANA]	Synthase

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2424	360	RECEPTOR KINASE, PUTATIVE SIMILAR TO CLVI RECEPTOR KINASE GB:AAB58929 GI:2160756 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2437	361	SENSORY TRANSDUCTION HISTIDINE KINASE SIMILAR TO GB:AAD21777; SIMILAR TO ESTS GB AA712891 AND GB AA042438[PUTATIVE]	Kinase, Protein
2474	362	LIPASE SIMILAR TO HYPOTHETICAL PROTEIN GB:AAF24946 GI:6693020 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Lipase
2494	363	POLYGALACTURONASE GB: AAC04907 GI:2924778 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Glycosylase
2510	364	IRON/ASCORBATE OXIDOREDUCTASE FAMILY	Reductase
2516	365	POLY A POLYMERASE FAMILY MEMBERS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Polymerase
2525	366	STEROID SULFOTRANSFERASE, PUTATIVE SIMILAR TO STEROID SULFOTRANSFERASE 3 GI:3420008 FROM [BRASSICA NAPUS]	Transferases
2529	367	PURINE PERMEASE, PUTATIVE SIMILAR TO PURINE PERMEASE GI:7620007 FROM [ARABIDOPSIS THALIANA]	Transporter
2530	368	PURINE PERMEASE IDENTICAL TO PURINE PERMEASE GI:7620007 FROM [ARABIDOPSIS THALIANA]	Transporter
2542	369	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:4105699 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2547	370	WALL-ASSOCIATED KINASE 1, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 1 GI:3549626 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2552	371	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:4105699 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2565	372	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase

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2566	373	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2567	374	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2568	375	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2569	376	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2571	377	LIPASE, PUTATIVE SIMILAR TO LIPASE GB:AAA93262 GI:1145627 [ARABIDOPSIS THALIANA]	Lipase
2572	378	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2574	379	LIPASE IDENTICAL TO LIPASE GB:AAA93262 GI:1145627 [ARABIDOPSIS THALIANA] (FEBS LETT. 377 (3), 475-480 (1995))	Lipase
2575	380	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHRANILATE N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE GB:Z84384 GI:2239084 [DIANTHUS CARYOPHYLLUS]	N-Transfases
2617	381	BETA,1,3 GLUCANASE, PUTATIVE SIMILAR TO GI:7414433 FROM [PISUM SATIVUM]	Glycosylase
2620	382	PHOSPHORIBOSYLANTHRANILATE ISOMERASE IDENTICAL TO GI:619749 FROM [ARABIDOPSIS THALIANA] (PLANT CELL 7 (4), 447-461 (1995))	Isomerase
2644	383	REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO GI:976278 FROM [ARABIDOPSIS THALIANA]	Transcriptase
2645	384	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase

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2646	385	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
2651	386	RECEPTOR-LIKE SERINE/THREONINE KINASE (RFK1), PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE (RFK1) GI:9972369 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2652	387	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2653	388	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2654	389	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE, 5' PARTIAL SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2660	390	PHENYLALANINE HYDROXYLASE GI:476740 FROM [PSEUDOMONAS AERUGINOSA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Hydroxylase
2663	391	ESTERASE GI:4191785 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Esterase
2686	392	BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO GI:4097948 FROM [ORYZA SATIVA] (GENE 223 (1-2), 311-320 (1998))	Glycosylase
2688	393	9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO 9-CIS-EPOXYCAROTENOID DIOXYGENASE GI:6715257 FROM [PHASEOLUS VULGARIS]	Oxygenases
2689	394	DIADENOSINE 5,5'-P1,P4-TETRAPHOSPHATE HYDROLASE, PUTATIVE SIMILAR TO DIADENOSINE 5,5'-P1,P4-TETRAPHOSPHATE HYDROLASE GI:1888556 FROM [LUPINUS ANGUSTIFOLIUS]	Hydrolase
2705	395	CYCLING-ASSOCIATED KINASE GI:1902912 FROM [RATTUS NORVEGICUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein

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2707	396	HYDROLASE GI:7270684 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Hydrolase
2710	397	PECTATE LYASE, PUTATIVE CONTAINS PFAM PROFILE: PF00544: PECTATE LYASE	Lyase
2712	398	LIPASE, PUTATIVE CONTAINS PFAM PROFILE: PF01764: LIPASE	Lipase
2714	399	REVERSE TRANSCRIPTASES, POSSIBLE PSEUDOGENE[HYPOTHETICAL PROTEIN SIMILAR TO], PORTIONS OF LINE-ELEMENT	Transcriptase
2716	400	ABC TRANSPORTER, PUTATIVE CONTAINS PFAM PROFILE: PF00005: ABC TRANSPORTER	Transporter
2717	401	ABC TRANSPORTER, PUTATIVE CONTAINS PFAM PROFILE: PF00005: ABC TRANSPORTER	Transporter
2725	402	FERRODOXIN NADP OXIDOREDUCTASE, PUTATIVE SIMILAR TO FERRODOXIN NADP OXIDOREDUCTASE GB:X99419 GI:1480346 FROM [PISUM SATIVUM]	Reductase
2727	403	UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE GB:AAB81683 GI:2564114 FROM [VITIS VINIFERA]	Transferases
2731	404	SERINE/THREONINE PROTEIN KINASE CONTAINS EUKARYOTIC PROTEIN KINASE DOMAIN PF 00069, SIMILAR TO GB:AAB47421[PUTATIVE]	Kinase, Protein
2744	405	RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase
2745	406	RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase

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2746	407	RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase
2747	408	RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase
2748	409	RETICULINE OXIDASE-LIKE PROTEIN SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase
2750	410	RETICULINE OXIDASE-LIKE PROTEIN, 3' PARTIAL SIMILAR TO GB:P30986 FROM [ESCHSCHOLZIA CALIFORNICA] (BERBERINE BRIDGE-FORMING ENZYME), ESTS GB F19886, GB Z30784 AND GB Z30785 COME FROM THIS GENE[PUTATIVE]	Oxidase
2759	411	PEROXIDASE SIMILAR TO CATIONIC PEROXIDASE (GI 1232069); SIMILAR TO EST GB AI100412[PUTATIVE]	Oxidase
2762	412	VACUOLAR SORTING RECEPTOR SIMILAR TO (GI 3033390); SIMILAR TO EST DBJ C72582[PUTATIVE]	Receptor
2784	413	POTASSIUM TRANSPORTER SIMILAR TO POTASSIUM TRANSPORTER GB:AAB87687[PUTATIVE]	Transporter
2794	414	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE ALMOST IDENTICAL TO GB:P52422 FROM [ARABIDOPSIS THALIANA], INVOLVED WITH PURINE BIOSYNTHESIS[PUTATIVE]	Transferases
2795	415	ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE ALMOST IDENTICAL TO GB X71364 GENE FOR ASPARTATE KINASE HOMOSERINE DEHYDROGENASE FROM ARABIDOPSIS THALIANA[PUTATIVE]	Dehydrogenases

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2798	416	IRON-REGULATED TRANSPORTER PROTEIN, PUTATIVE SIMILAR TO IRON-REGULATED TRANSPORTER 2 GB:AAD30549 GI:4836773 FROM [LYCOPERSICON ESCULENTUM]	Transporter
2814	417	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
2821	418	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, PUTATIVE SIMILAR TO N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [IPOMOEA BATATAS] GI:6469032	Transferases
2836	419	COPPER AMINE OXIDASE, PUTATIVE SIMILAR TO COPPER AMINE OXIDASE GI:4651202 FROM [PISUM SATIVUM]	Oxidase
2838	420	COPPER AMINE OXIDASE, PUTATIVE SIMILAR TO COPPER AMINE OXIDASE GI:685197 FROM [PISUM SATIVUM]	Oxidase
2853	421	AMINO ACID PERMEASE, PUTATIVE CONTAINS PFAM PROFILE: PF00324: AMINO ACID PERMEASE	Transporter
2854	422	AMINO ACID PERMEASE, PUTATIVE CONTAINS PFAM PROFILE: PF00324: AMINO ACID PERMEASE	Transporter
2857	423	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (AT-IE) IDENTICAL TO PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (AT-IE) [ARABIDOPSIS THALIANA] GI:3461884 (PLANT PHYSIOL. 118 (1), 275-283 (1998))	Hydrolase
2859	424	MAJOR INTRINSIC PROTEIN, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00861: MIP FAMILY CHANNEL PROTEINS	Channel
2860	425	MAJOR INTRINSIC PROTEIN, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00861: MIP FAMILY CHANNEL PROTEINS	Channel
2865	426	TERPENE SYNTHASE FAMILY PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF01397: TERPENE SYNTHASE FAMILY	Synthase

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2873	427	SECRETORY CARRIER MEMBRANE PROTEIN, PUTATIVE SIMILAR TO SECRETORY CARRIER MEMBRANE PROTEIN GI:7109228 FROM [ARABIDOPSIS THALIANA]	Transporter
2874	428	PHOSPHORIBULOKINASE PRECURSOR IDENTICAL TO PHOSPHORIBULOKINASE PRECURSOR GB:P25697 GI:125576 FROM [ARABIDOPSIS THALIANA]	Kinase
2878	429	PINORESINOL-LARICIRESINOL REDUCTASE, PUTATIVE SIMILAR TO PINORESINOL-LARICIRESINOL REDUCTASE GB:AAF63508 GI:7542583 FROM [THUJA PLICATA]	Reductase
2883	430	OBTUSIFOLIOL 14-ALPHA-DEMETHYLASE (CYP51) GB:Y09292 GI:1707854 FROM [TRITICUM AESTIVUM], CONTAINS SIMILARITY TO	Methylase
2884	431	ENDOXYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO ENDOXYLOGLUCAN TRANSFERASE GB:AAD45125 GI:5533313 FROM [ARABIDOPSIS THALIANA]	Transferases
2885	432	CELLULOSE SYNTHASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB:BAB09693 GI:9759258 FROM [ARABIDOPSIS THALIANA]	Synthase
2887	433	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE IDENTICAL TO GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE GB:Q43307 FROM [ARABIDOPSIS THALIANA]	Transferases
2897	434	L-GULONOLACTONE OXIDASE GB:J03536 GI:204149 FROM [RATTUS NORVEGICUS] UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Oxidase
2898	435	L-GULONOLACTONE OXIDASE GB:J03536 GI:204149 FROM [RATTUS NORVEGICUS] UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Oxidase
2902	436	OXIDASE; PUTATIVE SIMILAR TO OXIDASE GB:AAA32870 GI:166876 FROM [ARABIDOPSIS THALIANA]	Oxidase

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2930	437	PROTEIN KINASE, PUTATIVE IDENTICAL TO BHLH PROTEIN GB:CAA67885 GI:1465368 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
2938	438	PROTEIN PHOSPHATASE 2C GB:CAA72341 GI:2582800 FROM [MEDICAGO SATIVA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Phosphatase
2952	439	BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO BETA-1,3-GLUCANASE PRECURSOR GI:4097948 FROM [ORYZA SATIVA]	Glycosylase
2955	440	STARCH SYNTHASE, PUTATIVE SIMILAR TO STARCH SYNTHASE GI:21613 FROM [SOLANUM TUBEROSUM]	Synthase
2965	441	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO][PUTATIVE]	Transcriptase
2968	442	CATECHOL O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO CATECHOL O-METHYLTRANSFERASE GI:4808524 FROM [THALICTRUM TUBEROSUM]	Transferases
2981	443	BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO ENDO-1,3-BETA-GLUCANASE GB: AAC39322 GI:2735502 FROM [HORDEUM VULGARE]	Glycosylase
2985	444	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
2999	445	NITRATE TRANSPORTER NTL1, PUTATIVE SIMILAR TO GI:3377517 FROM [ARABIDOPSIS THALIANA]	Transporter
3015	446	EPIDERMAL GROWTH FACTOR RECEPTOR-LIKE PROTEIN GB:AAB31972 GI:9256501 FROM [XIPHOPHORUS MACULATUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Receptor
3017	447	DISEASE RESISTANCE PROTEIN, PUTATIVE SIMILAR TO RECEPTOR KINASE-LIKE PROTEIN GB:AAB82755 GI:2586083 FROM [ORYZA LONGISTAMINATA] (SCIENCE 270 (5243), 1804-1806 (1995))	Kinase, Protein
3024	448	TERPENE SYNTHASE, PUTATIVE SIMILAR TO DELTA-CADINENE SYNTHASE ISOZYME A GB:Q43714 FROM [GOSSYPIUM ARBOREUM]	Synthase

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3050	449	POLYNEURIDINE ALDEHYDE ESTERASE, PUTATIVE SIMILAR TO POLYNEURIDINE ALDEHYDE ESTERASE GI:6651393 FROM [RAUVOLFIA SERPENTINA]	Esterase
3062	450	RECEPTOR PROTEIN KINASE-LIKE PROTEIN GI:10177178 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
3066	451	PSEUDOURIDINE SYNTHASES[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO	Synthase
3072	452	SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA]	Kinase, Protein
3079	453	RECEPTOR-LIKE PROTEIN KINASE GI:6979335 FROM [ORYZA SATIVA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
3082	454	PEROXIDASE, PUTATIVE SIMILAR TO GI:1199777 FROM [POPULUS NIGRA]	Oxidase
3087	455	DNA POLYMERASE I, PUTATIVE SIMILAR TO GI:4090935 FROM [RHODOTHERMUS SP. 'ITI 518']	Polymerase
3091	456	PROTEIN KINASE DOMAIN (2 COPIES),PF00560 LEUCINE RICH REPEAT (17 COPIES)	Kinase, Protein
3099	457	PEROXIDASE ATP13A, PUTATIVE SIMILAR TO GB:CAA67312 FROM [ARABIDOPSIS THALIANA]	Oxidase
3121	458	PROTEIN PHOSPHATASE TYPE 2C, PUTATIVE SIMILAR TO GB:AAD17805 FROM [LOTUS JAPONICUS]. (PROC. NATL. ACAD. SCI. U.S.A. 96 (4), 1738-1743 (1999))	Phosphatase
3143	459	HYOSCYAMINE 6-DIOXYGENASE HYDROXYLASE, PUTATIVE SIMILAR TO HYOSCYAMINE 6- DIOXYGENASE HYDROXYLASE GB:P24397 FROM [HYOSCYAMUS NIGER]	Oxygenases
3199	460	PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES	Kinase, Protein
3214	461	TREHALOSE-PHOSPHATASE, PUTATIVE CONTAINS TIGRFAM PROFILE: TIGR00685: TREHALOSE- PHOSPHATASE	Phosphatase

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3239	462	ACETYL-COA CARBOXYLASE, PUTATIVE SIMILAR TO GI:1100253 FROM [ARABIDOPSIS THALIANA]	Carboxylase
3244	463	ADENYLOSUCCINATE LYASE-LIKE PROTEIN SIMILAR TO SP:P44797 FROM [HAEMOPHILUS INFLUENZAE]	Lyase
3249	464	VANILLOID RECEPTOR-LIKE PROTEIN GB:AAD26363 FROM [HOMO SAPIENS][HYPOTHETICAL PROTEIN SIMILAR TO]	Receptor
3284	465	NON-LTR REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transcriptase
3290	466	BIOTIN HOLOCARBOXYLASE SYNTHETASE, PUTATIVE SIMILAR TO BIOTIN HOLOCARBOXYLASE SYNTHETASE GI:4874309 FROM [ARABIDOPSIS THALIANA]	Synthase
3340	467	PECTINESTERASE, PUTATIVE, 5' PARTIAL SIMILAR TO GI:1944574 FROM [LYCOPERSICON ESCULENTUM]	Esterase
3394	468	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS]	Glycosylase
3395	469	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS]	Glycosylase
3396	470	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:288611 FROM [ZEA MAYS]	Glycosylase
3413	471	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4006833 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
3418	472	STEROL GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO STEROL GLUCOSYLTRANSFERASE GI:4731867 FROM [DICTYOSTELIUM DISCOIDEUM]	Transferases
3427	473	HISTIDINE DECARBOXYLASE, PUTATIVE SIMILAR TO HISTIDINE DECARBOXYLASE GB:BAA78331 GI:4996105 FROM [BRASSICA NAPUS]	Decarboxylase
3435	474	REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO REVERSE TRANSCRIPTASE GB:CAA73798 GI:2462134 FROM [BETA VULGARIS]	Transcriptase

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3439	475	STEAROYL ACYL CARRIER PROTEIN DESATURASE, PUTATIVE SIMILAR TO STEAROYL ACYL CARRIER PROTEIN DESATURASE LLDD3A20 GB: AAD28287 GI:4704824 FROM [LUPINUS LUTEUS]	Desaturases
3455	476	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:4544460 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Transcriptase
3464	477	GIBBERELLIN 20-OXIDASE, PUTATIVE, 5' PARTIAL SIMILAR TO GIBBERELIN 20-OXIDASE GI:4164141 FROM [LACTUCA SATIVA]	Oxidase
3470	478	AMINO ACID PERMEASE, PUTATIVE ALMOST IDENTICAL TO AMINO ACID PERMEASE GI:608673 FROM [ARABIDOPSIS THALIANA]	Transporter
3471	479	GIBBERELLIN 20-OXIDASE, PUTATIVE SIMILAR TO GIBBERELIN 20-OXIDASE GI:4164141 FROM [LACTUCA SATIVA]	Oxidase
3497	480	PEROXIDASE ATP18A, 3' PARTIAL IDENTICAL TO GB:CAA67336 FROM [ARABIDOPSIS THALIANA]	Oxidase
3498	481	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GI:1617588 FROM [LYCOPERSICON ESCULENTUM]	Esterase
3537	482	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3746069 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
3544	483	PHYTOCHELATIN SYNTHETASE GI:3559805 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Synthase
3545	484	AAA-TYPE ATPASE-LIKE PROTEIN GI:9759053 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	ATPase
3564	485	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD21515 GI:4510429 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
3570	486	PROTEIN PHOSPHATASE 2C GB:AAD25933 GI:4587992 FROM [ARABIDOPSIS THALIANA]	Phosphatase

3578	487	ESTERASE GI:4335745 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Esterase
3597	488	LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA]	Transporter
3610	489	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB: AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
3632	490	DIOXYGENASE, PUTATIVE SIMILAR TO DIOXYGENASE GB: CAA70330 GI:1666096 FROM [MARAH MACROCARPUS]	Oxygenases
3643	491	POLYGALACTURONASE PG1, PUTATIVE SIMILAR TO GB: AAD46483 FROM [GLYCINE MAX] (MOL. PLANT MICROBE INTERACT. 12 (6), 490-498 (1999))	Glycosylase
3660	492	G PROTEIN COUPLED RECEPTOR IDENTICAL TO PUTATIVE G PROTEIN COUPLED RECEPTOR GI:2104224 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Receptor
3674	493	1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE [UNKNOWN PROTEIN CONTAINS SIMILARITY TO]	Deaminase
3680	494	PROTEIN KINASE, PUTATIVE CONTAINS SIMILARITY TO MANY PREDICTED PROTEIN KINASES	Kinase, Protein
3696	495	LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA]	Transporter
3703	496	LECTIN RECEPTOR KINASE, PUTATIVE SIMILAR TO LECTIN RECEPTOR KINASE GI:1769897 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
3711	497	TERPENE CYCLASE, PUTATIVE SIMILAR TO TERPENE CYCLASE GI:9293912 FROM [ARABIDOPSIS THALIANA]	Cyclase
3712	498	TERPENE CYCLASE, PUTATIVE SIMILAR TO TERPENE CYCLASE GI:9293912 FROM [ARABIDOPSIS THALIANA]	Cyclase

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3715	499	CHORISMATE SYNTHASE, PUTATIVE SIMILAR TO CHORISMATE SYNTHASE GI:452796 FROM [SYNECHOCYSTIS SP.]	Synthase
3720	500	FLAVIN-CONTAINING MONOOXYGENASE, PUTATIVE SIMILAR TO FLAVIN-CONTAINING MONOOXYGENASE 4 GI:31429 FROM [HOMO SAPIENS]	Oxygenases
3736	501	LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
3753	502	RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
3764	503	FLAVONOL SYNTHASE, PUTATIVE SIMILAR TO FLAVONOL SYNTHASE GI:311657 FROM [PETUNIA HYBRIDA]	Synthase
3776	504	GERANYL GERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYL GERANYL PYROPHOSPHATE SYNTHASE GB:BAA23157 GI:2578822 FROM [ARABIDOPSIS THALIANA]	Synthase
3780	505	PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GB:P80679 FROM [ARMORACIA RUSTICANA]	Oxidase
3787	506	ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Esterase
3788	507	ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA; UNKNOWN PROTEIN SIMILAR TO]	Esterase
3789	508	ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA]ESTERASE GB:AAD17422 GI:4335745 FROM [ARABIDOPSIS THALIANA; UNKNOWN PROTEIN SIMILAR TO UNKNOWN PROTEIN SIMILAR TO]	Esterase
3793	509	FUCOSYLTRANSFERASE C3 PROTEIN, PUTATIVE SIMILAR TO FUCOSYLTRANSFERASE C3 PROTEIN GB:CAB52254 GI:5702039 FROM [VIGNA RADIATA]	Transferases

3796	510	MAP3K-LIKE PROTEIN KINASE GI:4006878 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
3801	511	GLUTAMINE AMIDOTRANSFERASES CLASS-II GLUTAMINE AMIDOTRANSFERASE CLASS-IHISTONE ACETYLTRANSFERASE HAT B HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00117 HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00310	Transferases
3803	512	NA+/H+ ANTIPORTER, PUTATIVE SIMILAR TO PROTEIN CONTAINED WITHIN GB:AE001273 FROM [CHLAMYDIA TRACHOMATIS]	Transporter
3808	513	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GI:860955 FROM [HYOSCYAMUS MUTICUS] (PLANT PHYSIOL. 109 (1), 253-260 (1995))	Transferases
3825	514	PHOSPHATIDYLINOSITOL 3-KINASE TOR1 GB:AAD16273 GI:4323240 FROM [FILOBASIDIUM NEOFORMANS], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Kinase
3828	515	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, PUTATIVE SIMILAR TO BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE GB:AAF07191 GI:6319165 FROM [SOLANUM TUBEROSUM]	Transferases
3835	516	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD25836 GI:4587608 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transcriptase
3856	517	FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE GB:U37838 GI:1052972 FROM [BETA VULGARIS]	Kinase
3873	518	UDP RHAMNOSE: ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP RHAMNOSE: ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE [PETUNIA X HYBRIDA] GI:397567	Transferases

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3876	519	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
3898	520	DNA POLYMERASE A FAMILY PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF00476: DNA POLYMERASE FAMILY A	Polymerase
3909	521	GIBBERELLIN 20-OXIDASE, PUTATIVE SIMILAR TO GIBBERELLIN 20-OXIDASE [TRITICUM AESTIVUM] GI:2222796	Oxidase
3912	522	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
3919	523	DNA POLYMERASE III, EPSILON SUBUNIT GI:8163241 FROM [CHLAMYDIA MURIDARUM][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Polymerase
3923	524	ANTHRANILATE SYNTHASE LARGE SUBUNIT GI:1374671 FROM [BUCHNERA APHIDICOLA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Synthase
3932	525	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
3952	526	CINNAMYL ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO GB:X88797 FROM [EUCALYPTUS GUNNII] (PLANT MOL. BIOL. 36 (5), 755-765 (1998))	Dehydrogenases
3968	527	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE, PUTATIVE SIMILAR TO PIR:T06460 FROM [PISUM SATIVUM]	Transferases
3983	528	NADP-SPECIFIC GLUTATAMATE DEHYDROGENASE, PUTATIVE SIMILAR TO NADP-SPECIFIC GLUTATAMATE DEHYDROGENASE (NADP-GDH) SP:P28724 [GIARDIA LAMBLIA (GIARDIA INTESTINALIS)]	Dehydrogenase
3986	529	REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase
3987	530	IAA-ALA HYDROLASE (IAR3) IDENTICAL TO IAA-ALA HYDROLASE (IAR3) [ARABIDOPSIS THALIANA] GI:3421384	Hydrolase

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3989	531	AUXIN CONJUGATE HYDROLASE (ILLS) IDENTICAL TO AUXIN CONJUGATE HYDROLASE [ARABIDOPSIS THALIANA] (ILLS) GI:5725649; CONTAINS NONCONSENSUS AT ACCEPTOR SPLICE SITE AT EXON3	Hydrolase
3990	532	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT	Kinase, Protein
3991	533	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT	Kinase, Protein
3992	534	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT	Kinase, Protein
3996	535	LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4001	536	LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GI:1321686 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4011	537	CAFFEIC ACID O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO CAFFEIC ACID O-METHYLTRANSFERASE GI:5031492 FROM [OCIMUM BASILICUM]	Transferases
4039	538	PROTEIN KINASE, PUTATIVE SIMILAR TO GI:7573596 FROM [POPULUS NIGRA]	Kinase, Protein
4041	539	PROTEIN KINASE, PUTATIVE SIMILAR TO GI:7573596 FROM [POPULUS NIGRA]	Kinase, Protein
4044	540	SHORT CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO GI:2739279 FROM [NICOTIANA TABACUM] (PLANT MOL. BIOL. 29 (5), 1027-1038 (1995))	Dehydrogenase

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4051	541	GLYCOSYL TRANSFERASE, PUTATIVE SIMILAR TO PFAM PROFILE: PF00534 GLYCOSYL TRANSFERASES GROUP 1	Transferases
4053	542	GLYCOSYL TRANSFERASES-LIKE PROTEIN GI:9294599 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Transferases
4065	543	SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA]	Kinase, Protein
4081	544	LYSOPHOSPHOLIPASE GI:1552244 FROM [RATTUS NORVEGICUS]; UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Lipase
4086	545	AB HYDROLASE DOMAIN	Hydrolase
4087	546	LIPASE SIMILAR TO MONOGLYCERIDE LIPASE GB:NP_035974 FROM [MUS MUSCULUS][PUTATIVE]	Lipase
4090	547	OXYGENASE OXIDOREDUCTASE SIMILAR TO ADVENTITIOUS ROOTING RELATED GB:CAA12386 FROM [MALUS DOMESTICA][PUTATIVE]	Reductase
4091	548	GIBBERELLIN 20-OXIDASE GB:1581592 FROM [ARABIDOPSIS THALIANA][PUTATIVE], OXIDOREDUCTASE SIMILAR TO	Oxidase
4092	549	OXYGENASE OXIDOREDUCTASE SIMILAR TO ADVENTITIOUS ROOTING RELATED GB:CAA12386 FROM [MALUS DOMESTICA][PUTATIVE]	Reductase
4093	550	GIBBERELLIN 20-OXIDASE GB:AAD42693 FROM [CITRULLUS LANATUS][PUTATIVE], OXIDOREDUCTASE SIMILAR TO	Oxidase
4104	551	PURPLE ACID PHOSPHATASE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 FROM [IPOMOEA BATATAS][PUTATIVE]	Phosphatase
4110	552	DEOXYOCTULONOSIC ACID SYNTHETASE SIMILAR TO 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLYLTRANSFERASE GB:P04951 FROM [ESCHERICHIA COLI][PUTATIVE]	Synthase

4117	553	PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES	Kinase, Protein
4118	554	PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES	Kinase, Protein
4119	555	PROTEIN KINASE, PUTATIVE SIMILAR TO MANY PREDICTED PROTEIN KINASES	Kinase, Protein
4143	556	PHOSPHOENOLPYRUVATE CARBOXYLASE 1, PUTATIVE SIMILAR TO PHOSPHOENOLPYRUVATE CARBOXYLASE 1 GI:2266947 FROM [GOSSYPIUM HIRSUTUM]	Carboxylase
4154	557	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4155	558	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4163	559	CHALCONE ISOMERASE, PUTATIVE SIMILAR TO GI:4126399 FROM [CITRUS SINENSIS]	Isomerase
4178	560	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GI:2853219 FROM [CARICA PAPAYA]	Transferases
4183	561	LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1, PUTATIVE SIMILAR TO GI:3360289 FROM [ZEA MAYS] (PLANT MOL. BIOL. 37 (5), 749-761 (1998))	Kinase, Protein
4184	562	LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1, PUTATIVE SIMILAR TO GI:3360289 FROM [ZEA MAYS] (PLANT MOL. BIOL. 37 (5), 749-761 (1998))	Kinase, Protein
4193	563	PECTIN METHYLESTERASE (PMEU1), PUTATIVE SIMILAR TO PECTIN METHYLESTERASE (PMEU1) GI:1222551 FROM [LYCOPERSICON ESCULENTUM]	Esterase
4194	564	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GI:732912 FROM [PHASEOLUS VULGARIS]	Esterase

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4202	565	LIPASE/HYDROLASE GI:9759145 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO	GDSL-like motif PROTEIN	Lipase
4203	566	LIPASE, PUTATIVE SIMILAR TO LIPASE GI:1145627 FROM [ARABIDOPSIS THALIANA]	GI:1145627	Lipase
4208	567	LIPASE, PUTATIVE SIMILAR TO LIPASE GI:1145627 FROM [ARABIDOPSIS THALIANA]	GI:1145627	Lipase
4278	568	NADH DEHYDROGENASE SUBUNIT 3 GI:7542364 FROM [PAGURUS LONGICARPUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	GI:7542364	Dehydrogenase
4286	569	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:9294282 FROM [ARABIDOPSIS THALIANA]	GI:9294282	Kinase, Protein
4298	570	GLYCOSYL TRANSFERASE GI:7021339 FROM [SINORHIZOBIUM MELILOTI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	GI:7021339	Transferases
4299	571	NADH DEHYDROGENASE SUBUNIT 6 GI:2660574 FROM [FICEDULA HYPOLEUCA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	GI:2660574	Dehydrogenase
4300	572	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GI:3785984 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	GI:3785984	Transcriptase
4315	573	BETA-FRUCTOFURANOSIDASE, PUTATIVE SIMILAR TO BETA-FRUCTOFURANOSIDASE GI:9294027 FROM [ARABIDOPSIS THALIANA]	GI:9294027	Glycosylase
4323	574	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	PF00069	Kinase, Protein
4332	575	LEUCOANTHOCYANIDIN DIOXYGENASE 2, PUTATIVE SIMILAR TO GI:5924383 FROM [DAUCUS CAROTA]	GI:5924383	Oxygenases
4351	576	TYROSINE PHOSPHATASE GB:AAF81798 GI:8926334 FROM [ORYZA SATIVA], SIMILAR TO PUTATIVE	GB:AAF81798	Phosphatase
4364	577	RECEPTOR KINASE, PUTATIVE SIMILAR TO CLV1 RECEPTOR KINASE GB:AAB58929 GI:2160756 FROM [ARABIDOPSIS THALIANA]	GB:AAB58929	Kinase, Protein

4375	578	H+/CA2+ ANTIPORTER, PUTATIVE SIMILAR TO H+/CA2+ EXCHANGER 2 GB:BAA75232 GI:4512263 FROM [IPOMOEA NIL]	Transporter
4376	579	H+/CA2+ ANTIPORTER, PUTATIVE SIMILAR TO H+/CA2+ EXCHANGER 2 GB:BAA75232 GI:4512263 FROM [IPOMOEA NIL]	Transporter
4389	580	CELLULOSE SYNTHASE CATALYTIC SUBUNIT, PUTATIVE SIMILAR TO GB:AAD39534 FROM [GOSSYPIUM HIRSUTUM]	Synthase
4396	581	SERINE ACETYLTRANSFERASE IDENTICAL TO GB:CAA84371 FROM [ARABIDOPSIS THALIANA] (EUR. J. BIOCHEM. 227 (1-2), 500-509 (1995))	Transferases
4417	582	WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4418	583	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI:2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4419	584	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT	Kinase, Protein
4436	585	3'-5' EXONUCLEASE, PUTATIVE CONTAINS PFAM PROFILE: PF01612: 3'-5' EXONUCLEASE	Nuclease
4464	586	TRIACYLGLYCEROL ACYLHYDROLASE GI:230348 FROM [RHIZOMUCOR MIEHEI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Hydrolase
4469	587	CHITINASE, PUTATIVE SIMILAR TO CHITINASE GI:17798 FROM [BRASSICA NAPUS]	Chitinase
4472	588	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE PGI... GI:5669846... FROM [GLYCINE MAX]	Glycosylase
4473	589	RECEPTOR-LIKE PROTEIN KINASE GI:7529754 FROM [ARABIDOPSIS THALIANA], SIMILAR TO	Kinase, Protein

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4480	590	PECTINACETYLESTERASE PRECURSOR, PUTATIVE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GI:1431629 FROM [VIGNA RADIATA]	Esterase
4512	591	ATP PHOSPHORIBOSYL TRANSFERASE IDENTICAL TO ATP PHOSPHORIBOSYL TRANSFERASE GI:6683617 FROM [ARABIDOPSIS THALIANA]	Transferases
4518	592	PHOSPHOGLYCERATE KINASE, PUTATIVE SIMILAR TO PHOSPHOGLYCERATE KINASE GI:155584 FROM [ZYMMOMONAS MOBILIS]	Kinase
4520	593	CARBONIC ANHYDRASE, PUTATIVE SIMILAR TO CARBONIC ANHYDRASE 1 GI:882241 FROM [FLAVERIA LINEARIS]	Anhydrase
4532	594	GLUTAMYL-TRNA REDUCTASE, PUTATIVE SIMILAR TO GLUTAMYL-TRNA REDUCTASE GI:1694925 FROM [CUCUMIS SATIVUS]	Reductase
4533	595	HEME OXYGENASE PLASTID, PUTATIVE SIMILAR TO PLASTID HEME OXYGENASE GI:4877397 FROM [ARABIDOPSIS THALIANA]	Oxygenases
4539	596	AMINO ACID PERMEASE I IDENTICAL TO AMINO ACID PERMEASE I GI:22641 FROM [ARABIDOPSIS THALIANA]	Transporter
4541	597	XYLAN ENDOHYDROLASE, PUTATIVE SIMILAR TO (1,4)-BETA-XYLAN ENDOHYDROLASE GI:5306060 FROM [TRITICUM AESTIVUM]	Hydrolase
4545	598	PEPTIDYL-PROLYL ISOMERASE, PUTATIVE SIMILAR TO PEPTIDYLPROLYL ISOMERASE GI:9294180 FROM [ARABIDOPSIS THALIANA]	Isomerase
4553	599	XYLAN ENDOHYDROLASE ISOENZYME, PUTATIVE SIMILAR TO Xylan ENDOHYDROLASE ISOENZYME X-1 GI:1813594 FROM [HORDEUM VULGARE]	Hydrolase
4571	600	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GB:AAF29773 GI:6856103 FROM [GOSSYPIUM HIRSUTUM]	Transferases
4573	601	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE S-TRANSFERASE GI:2190991 FROM [AEGILOPS TAUSCHII]	Transferases

4578	602	OLIGOPEPTIDE TRANSPORTER, PUTATIVE SIMILAR TO OLIGOPEPTIDE TRANSPORTER GI:510238 FROM [ARABIDOPSIS THALIANA]	Transporter
4617	603	POTASSIUM TRANSPORTER, PUTATIVE SIMILAR TO POTASSIUM TRANSPORTER GI:2654088 FROM [ARABIDOPSIS THALIANA]	Transporter
4637	604	POLYGALACTURONASE ISOENZYME 1 BETA SUBUNIT, PUTATIVE SIMILAR TO POLYGALACTURONASE ISOENZYME 1 BETA SUBUNIT GI:1762585 FROM [LYCOPERSICON ESCULENTUM]	Glycosylase
4643	605	GALACTINOL SYNTHASE, PUTATIVE SIMILAR TO GALACTINOL SYNTHASE GI:5608497 FROM [AJUGA REPTANS]	Synthase
4645	606	GALACTINOL SYNTHASE, PUTATIVE SIMILAR TO GALACTINOL SYNTHASE GI:5608497 FROM [AJUGA REPTANS]	Synthase
4650	607	2-KETOCYCLOHEXANECARBOXYL-COA HYDROLASE GI:3243084 FROM [RHODOPSEUDOMONAS PALUSTRIS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Hydrolase
4653	608	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:9293940 FROM [ARABIDOPSIS THALIANA]	Glycosylase
4655	609	S-RIBONUCLEASE BINDING PROTEIN SBP1 GI:6760451 FROM [PETUNIA HYBRIDA]	Nuclease
4657	610	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:498278 FROM [PETUNIA INTEGRIFOLIA]	Kinase, Protein
4661	611	D-ALA,D-ALA LIGASE GI:6634594 FROM [STREPTOCOCCUS PNEUMONIAE][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Ligase
4674	612	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GI:2224910 FROM [DAUCUS CAROTA]	Kinase, Protein
4687	613	IRON-REGULATED TRANSPORTER SIMILAR TO IRON-REGULATED TRANSPORTER 1 GB:AAD30548 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE]	Transporter

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4689	614	GIBBERELLIN 20-OXIDASE SIMILAR TO GIBBERELLIN 20-OXIDASE GB:CAA58295 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Oxidase
4690	615	AMINOMETHYLTRANSFERASE GB:CAA20175 FROM [STREPTOMYCES COELICOLOR A3(2)]; HYPOTHETICAL PROTEIN PREDICTED BY GENSCAN+, SIMILAR TO	Transferases
4702	616	S-LINALOOL SYNTHASE, PUTATIVE SIMILAR TO S-LINALOOL SYNTHASE GI:1491939 FROM [CLARKIA BREWERI]	Synthase
4715	617	SECRETORY CARRIER MEMBRANE PROTEIN IDENTICAL TO SECRETORY CARRIER MEMBRANE PROTEIN GI:7109228 FROM [ARABIDOPSIS THALIANA]	Transporter
4717	618	LYSINE AND HISTIDINE SPECIFIC TRANSPORTER, PUTATIVE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GI:2576361 FROM [ARABIDOPSIS THALIANA]	Transporter
4726	619	RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [IPOMOEA TRIFIDA]	Kinase, Protein
4727	620	RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [IPOMOEA TRIFIDA]	Kinase, Protein
4728	621	SERINE/THREONINE KINASE GI:4585880 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Kinase, Protein
4729	622	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4730	623	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 GI:2662048 FROM [BRASSICA RAPA]	Kinase, Protein
4732	624	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4733	625	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4734	626	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein

4736	627	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4738	628	RECEPTOR PROTEIN KINASE (IRK1), PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE (IRK1) GI:836953 FROM [IPOMOEA TRIFIDA]	Kinase, Protein
4739	629	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4740	630	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4744	631	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GI:166692 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4748	632	SERINE/THREONINE PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE PROTEIN KINASE GI:1066501 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4750	633	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1783311 FROM [BRASSICA OLERACEA]	Kinase, Protein
4752	634	INOSINE-GUANOSINE NUCLEOSIDE TRANSPORTER GI:8272582 FROM [LEISHMANIA DONOVANI][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transporter
4756	635	CINEOLE SYNTHASE, PUTATIVE SIMILAR TO 1,8-CINEOLE SYNTHASE GI:3309117 FROM [SALVIA OFFICINALIS]	Synthase
4760	636	DIHYDROFLAVONOL 4-REDUCTASE, PUTATIVE SIMILAR TO DIHYDROFLAVONOL 4-REDUCTASE GI:1332411 FROM [ROSA HYBRIDA]	Reductase
4763	637	SERINE/THREONINE PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE PROTEIN KINASE GI:3080385 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4774	638	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GI:9294282 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4795	639	RECEPTOR-LIKE PROTEIN KINASE GI:3461841 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Kinase, Protein

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4796	640	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GI:9758833 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
4804	641	5'-ADENYLYLPHOSPHOSULFATE REDUCTASE, PUTATIVE SIMILAR TO 5'-ADENYLYLPHOSPHOSULFATE REDUCTASE GI:1336168 FROM [ARABIDOPSIS THALIANA]	Reductase
4810	642	PEROXIDASE ISOZYME GI:217933 FROM [ARMORACIA RUSTICANA] UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Oxidase
4823	643	ACC OXIDASE, PUTATIVE SIMILAR TO ACC OXIDASE GI:587086 FROM [BRASSICA OLERACEA]	Oxidase
4843	644	GLUCOSE 1-DEHYDROGENASE (AB000617); SIMILAR TO EST GB:T88100 SIMILAR TO OXIDOREDUCTASE-LIKE PROTEIN GB:CAB75763 GI:7019662 FROM [ARABIDOPSIS THALIANA][SIMILAR TO]	Dehydrogenases
4846	645	3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III (KAS III) IDENTICAL TO 3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III (KAS III) GB:CAA72385 GI:1888359 [ARABIDOPSIS THALIANA]	Synthase
4863	646	AMINE OXIDASE, PUTATIVE SIMILAR TO AMINE OXIDASE GB:AAD49420 GI:5733089 [CANAVALIA LINEATA]	Oxidase
4871	647	NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO MANY PREDICTED NON-LTR REVERSE TRANSCRIPTASES	Transcriptase
4872	648	O-METHYLTRANSFERASE 1, PUTATIVE SIMILAR TO GB:AAB96879 FROM [ARABIDOPSIS THALIANA] (BIOCHIM. BIOPHYS. ACTA 1353 (3), 199-202 (1997))	Transferases
4877	649	PROTEIN KINASE, PUTATIVE CONTAINS PROTEIN KINASE DOMAINS	Kinase, Protein
4878	650	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE, PUTATIVE SIMILAR TO GB:U35779 FROM [TRITICUM AESTIVUM] (PLANT MOL. BIOL. 31 (5), 1009-1020 (1996))	Synthase

4896	651	CAFFEIC O-METHYLTRANSFERASE, PUTATIVE SIMILAR TO GI:602587 FROM [PRUNUS DULCIS] (PLANT PHYSIOL. 108, 1341-1341 (1995))	Transferases
4921	652	GLUCOSE 1-DEHYDROGENASE GB:P40288 FROM [BACILLUS MEGATERIUM], REDUCTASE, PUTATIVE SIMILAR TO	Dehydrogenases
4926	653	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT	Kinase, Protein
4933	654	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
4948	655	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE- 2,6-DIAMINOPIMELATE LIGASE SIMILAR TO UDP-N- ACETYLMURAMOYLALANYL-D-GLUTAMATE-2,6- DIAMINOPIMELATE LIGASE (MURE) GB:S40595 [ESCHERICHIA COLI][PUTATIVE]	Ligase
4956	656	AMINOPEPTIDASE SIMILAR TO AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) GB:P04825 [ESCHERICHIA COLI]; CONTAINS PFAM PROFILE: PF00099 ZINC-BINDING METALLOPROTEASE DOMAIN[PUTATIVE]	Protease
4970	657	MONODEHYDROASCORBATE REDUCTASE SIMILAR TO MONODEHYDROASCORBATE REDUCTASE GB:AAD28178 [BRASSICA JUNCEA][PUTATIVE]	Reductase
5024	658	PEPTIDE TRANSPORTER, PUTATIVE PREDICTED BY GENEMARK.HMM	Transporter
5049	659	BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA- 1,3-GLUCANASE GI:8843743 FROM [ARABIDOPSIS THALIANA]	Glycosylase
5059	660	RNA POLYMERASE SIGMA-SUBUNIT IDENTICAL TO PLASTID RNA POLYMERASE SIGMA-SUBUNIT GI:2398851 FROM [ARABIDOPSIS THALIANA]	Polymerase
5064	661	RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO RHAMNOSYLTRANSFERASE GI:454252 FROM [PETUNIA HYBRIDA]	Transferases

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5065	662	ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE GI:397567 FROM [PETUNIA HYBRIDA]	Transferases
5070	663	GAMMA-TOCOPHEROL METHYLTRANSFERASE ALMOST IDENTICAL TO GAMMA-TOCOPHEROL METHYLTRANSFERASE GI:4106538 FROM [ARABIDOPSIS THALIANA]	Transferases
5091	664	SERINE THREONINE KINASE GI:166813 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
5096	665	ASPARTYL PROTEASE GI:6728988 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Protease
5097	666	SERINE THREONINE KINASE GI:166813 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Kinase, Protein
5103	667	XYLOGLUCAN ENDOTRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDOTRANSGLYCOSYLASE I GI:3901012 FROM [FAGUS SYLVATICA]	Glycosylase
5114	668	ANTIGEN RECEPTOR, PUTATIVE SIMILAR TO ANTIGEN RECEPTOR GI:3982955 FROM [GINGLYMOSTOMA CIRRATUM]	Receptor
5123	669	CARNITINE RACEMASE LIKE PROTEIN GI:7268149 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Epimerase
5128	670	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:2605891 FROM [LYCOPERSICON ESCULENTUM]	Glycosylase
5129	671	INOSITOL POLYPHOSPHATE 5'-PHOSPHATASE GI:3212848 FROM [ARABIDOPSIS THALIANA], SIMILAR TO PUTATIVE	Phosphatase
5134	672	SERINE PROTEASE DO, PUTATIVE SIMILAR TO PROTEASE DO (HTRA) SP:P09376 [ESCHERICHIA COLI]	Protease

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5135	673	SERINE PROTEASE DO, PUTATIVE SIMILAR TO PROTEASE DO (HTRA) SP:P09376 [ESCHERICHIA COLI]	Protease
5150	674	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE I [BRASSICA RAPA] GB:BAA23676	Kinase, Protein
5151	675	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE I [BRASSICA RAPA] GB:BAA23676	Kinase, Protein
5166	676	GLUTAMATE DECARBOXYLASE (GAD), PUTATIVE SIMILAR TO GLUTAMATE DECARBOXYLASE (GAD) GI:294111 FROM [PETUNIA HYBRIDA]	Decarboxylase
5171	677	TERPENE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF01397: TERPENE SYNTHASE FAMILY	Synthase
5182	678	OXIDOREDUCTASE, PUTATIVE CONTAINS PFAM PROFILE: PF01408: OXIDOREDUCTASE, GFO/IDH/MOCA FAMILY	Reductase
5184	679	RECEPTOR PROTEIN KINASE (TMK1), PUTATIVE SIMILAR TO PUTATIVE RECEPTOR PROTEIN KINASE (TMK1) [ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)] SP:P43298	Kinase, Protein
5194	680	BETA-1,3-GLUCANASE PRECURSOR, PUTATIVE SIMILAR TO GI:4097948 FROM [ORYZA SATIVA] (GENE 223 (1-2), 311-320 (1998))	Glycosylase
5212	681	FRUCTOKINASE, PUTATIVE SIMILAR TO FRUCTOKINASE [LYCOPERSICON ESCULENTUM] GI:2102691	Kinase
5215	682	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
5221	683	FORMYL TRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF00551: FORMYL TRANSFERASE	Transferases
5226	684	SUCROSE-PROTON SYMPORTER, 5' PARTIAL SIMILAR TO C-TERM OF SUCROSE-PROTON SYMPORTER [ARABIDOPSIS THALIANA] GI:407094	Transporter
5248	685	CINNAMYL ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO CINNAMYL ALCOHOL DEHYDROGENASE [EUCALYPTUS GUNNII] GI:1143445	Dehydrogenases

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5251	686	RECEPTOR PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILES: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN, MULTIPLE PF00560: LEUCINE RICH REPEAT	Kinase, Protein
5256	687	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069: EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
5259	688	RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5260	689	RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5261	690	RECEPTOR SERINE/THREONINE KINASE PR5K, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5K GI:1235680 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5266	691	KINASE, PUTATIVE SIMILAR TO LEAF RUST RESISTANCE KINASE LR10 GI:1680685 FROM [TRITICUM AESTIVUM]	Kinase, Protein
5267	692	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:5523856 FROM [HORDEUM VULGARE]	Kinase, Protein
5275	693	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL UNIT, PUTATIVE SIMILAR TO RIBULOSE-BISPHOSPHATE CARBOXYLASE SMALL UNIT GI:406726 FROM [BRASSICA NAPUS]	Carboxylase
5292	694	GLYOXAL OXIDASE (GLX1), PUTATIVE SIMILAR TO GLYOXAL OXIDASE (GLX1) GI:1050301 FROM [PHANEROCHAETE CHRYSOSPORIUM]	Oxidase
5309	695	PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN; IDENTICAL TO GB: AAC18787 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase, Protein

5313	696	RECEPTOR-LIKE PROTEIN KINASE GI:4262228 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Kinase, Protein
5314	697	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE 1 GI:9294449 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5325	698	AMINO ACID PERMEASE SIMILAR TO LYSINE AND HISTIDINE SPECIFIC TRANSPORTER GB: AAC49885 [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
5330	699	AMINO ACID PERMEASE, PUTATIVE SIMILAR TO AMINO ACID PERMEASE 1 GB: AAB48944 GI:976402 FROM [NICOTIANA SYLVESTRIS]	Transporter
5341	700	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE GB:CAA66376 GI:1321686 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5344	701	ENDOCHITINASE, PUTATIVE SIMILAR TO PECTATE LYASE 1 GB:AAF19195 GI:6606532 FROM [MUSA ACUMINATA]	Chitinase
5346	702	ABC TRANSPORTER SIMILAR TO TERMINAL EAR1 GB:AAC39463 GI:3153237 FROM [ZEA MAYS] (NATURE 393 (6681), 166-168 (1998))[PUTATIVE]	Transporter
5358	703	N-ACETYLGLUCOSAMINYLTRANSFERASE III GB: AAC53064 [MUS MUSCULUS], UNKNOWN PROTEIN SIMILAR TO	Transferases
5368	704	S-ADENOSYL-L-METHIONINE:TRANS-CAFFEOYL-COENZYME A 3-O-METHYLTRANSFERASE SIMILAR TO S-ADENOSYL-L-METHIONINE:TRANS-CAFFEOYL-COENZYME A 3-O-METHYLTRANSFERASE GB:AAA62426 [ARABIDOPSIS THALIANA] (FUNCTION=DISEASE RESISTANCE)[PUTATIVE]	Transferases
5369	705	S-ADENOSYL-L-METHIONINE:TRANS-CAFFEOYL-COENZYME A 3-O-METHYLTRANSFERASE SIMILAR TO S-ADENOSYL-L-METHIONINE:TRANS-CAFFEOYL-COENZYME A 3-O-METHYLTRANSFERASE GB:AAA62426 [ARABIDOPSIS THALIANA] (FUNCTION=DISEASE RESISTANCE)[PUTATIVE]	Transferases

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5370	706	PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) IDENTICAL TO PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) GB:AJ000539	Synthase
5371	707	HYDROXYPYRUVATE REDUCTASE (HPR) IDENTICAL TO HYDROXYPYRUVATE REDUCTASE (HPR) GB:D85339 [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL 1997 APR;38(4):449-55)	Reductase
5374	708	S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE SIMILAR TO S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE GB:AAF00108 [CLARKIA BREWERI] (ENZYME INVOLVED IN FLORAL SCENT PRODUCTION AND PLANT DEFENSE)[PUTATIVE]	Transferases
5399	709	BIFUNCTIONAL NUCLEASE SIMILAR TO BIFUNCTIONAL NUCLEASE GB:AAD00694 FROM [ZINNIA ELEGANS][PUTATIVE]	Nuclease
5410	710	RECEPTOR KINASE SIMILAR TO RECEPTOR KINASE GB:AAA33715 FROM [PETUNIA INTEGRIFOLIA][PUTATIVE]	Kinase, Protein
5411	711	PROTEIN PHOSPHATASE SIMILAR TO PROTEIN PHOSPHATASE-2C GB: AAC36697 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE]	Phosphatase
5412	712	ASPARAGINYL-TRNA SYNTHETASE SIMILAR TO SYNC1 PROTEIN GB:AAD46681[PUTATIVE]	Synthase
5416	713	TRNA ISOPENTENYL TRANSFERASE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GB:AAF00582 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF01715 IPP TRANSFERASE (TRNA DELTA(2)-ISOPENTENYL PYROPHOSPHATE TRANSFERASE)[PUTATIVE]	Transferases
5424	714	CINNAMOYL COA REDUCTASE GB:CAA12276 [POPULUS BALSAMIFERA SUBSP. TRICHOCARPA], ALDEHYDE REDUCTASE GB:AAD53967 [VIGNA RADIATA], DIHYDROFLAVONOL 4-REDUCTASE GB:BAA12723 [ROSA HYBRIDA][PUTATIVE]	Reductase

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5439	715	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE 1 GB:BAA94509 GI:7573596 FROM [POPULUS NIGRA]	Kinase, Protein
5441	716	ATPASE, PUTATIVE SIMILAR TO CHROMAFFIN GRANULE ATPASE II GB:AAD03352 GI:4115341 FROM [BOS TAURUS]	ATPase
5442	717	CYTIDINE AND DEOXYCYTIDYLATE DEAMINASE ZINC-BINDING REGION [UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF00383]	Deaminase
5446	718	PHOSPHOENOLPYRUVATE CARBOXYLASE SIMILAR TO PHOSPHOENOLPYRUVATE CARBOXYLASE GB:CAA11415 [BRASSICA JUNCEA]; CONTAINS PFAM PROFILE: PF00311 PHOSPHOENOLPYRUVATE CARBOXYLASE[PUTATIVE]	Carboxylase
5453	719	PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5455	720	PEROXIDASE ATP23A IDENTICAL TO PEROXIDASE ATP23A GB:CAA70035 [ARABIDOPSIS THALIANA]	Oxidase
5458	721	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLIC ACID SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE, MENAQINONE BIOSYNTHESIS PROTEIN SIMILAR TO MENAQINONE BIOSYNTHESIS PROTEIN GB:P23970 [BACILLUS SUBTILIS]; PFAM HMM HIT: [PUTATIVE]	Synthase
5482	722	DIHYDROPTERIN PYROPHOSPHOKINASE, PUTATIVE SIMILAR TO DIHYDROPTERIN PYROPHOSPHOKINASE GI:1934971 FROM [PISUM SATIVUM]	Kinase
5483	723	FRUCTOKINASE SIMILAR TO FRUCTOKINASE GB:AAB57733 [LYCOPERSICON ESCULENTUM][PUTATIVE]	Kinase
5487	724	POLYNEURIDINE ALDEHYDE ESTERASE, PUTATIVE SIMILAR TO POLYNEURIDINE ALDEHYDE ESTERASE GI:6651393 FROM [RAUVOLFIA SERPENTINA]	Esterase
5490	725	RECEPTOR-LIKE PROTEIN KINASE SIMILAR TO PROTEIN KINASE GB:AAD11518 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase, Protein

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5499	726	CHORISMATE MUTASE, PUTATIVE CONTAINS PFAM PROFILE: PF01817: CHORISMATE MUTASE	Mutase
5525	727	STEROL DESATURASE CONTAINS PFAM PROFILE: PF01598 STEROL DESATURASE[PUTATIVE]	Desaturases
5533	728	HEME OXYGENASE SIMILAR TO HEME OXYGENASE GB:AAD22107 [ARABIDOPSIS THALIANA][PUTATIVE]	Oxygenases
5534	729	PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5544	730	ALPHA-AMYLASE SIMILAR TO ALPHA-AMYLASE GB:AAA91884 [SOLANUM TUBEROSUM][PUTATIVE]	Glycosylase
5546	731	NITRATE TRANSPORTER (NTL1) IDENTICAL TO NITRATE TRANSPORTER (NTL1) GB: AAC28086 [ARABIDOPSIS THALIANA]	Transporter
5547	732	PEPTIDE TRANSPORTER SIMILAR TO PEPTIDE TRANSPORTER GB: AAC32034 [HORDEUM VULGARE][PUTATIVE]	Transporter
5548	733	PEPTIDE TRANSPORTER SIMILAR TO PEPTIDE TRANSPORTER GB: AAC32034 [HORDEUM VULGARE][PUTATIVE]	Transporter
5552	734	PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5553	735	GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA09188 [ALOPECURUS MYOSUROIDES][PUTATIVE]	Transferases
5554	736	GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA09188 [ALOPECURUS MYOSUROIDES][PUTATIVE]	Transferases
5555	737	PECTIN METHYLESTERASE SIMILAR TO PECTIN METHYLESTERASE GB:CAA96435 [NICOTIANA PLUMBAGINIFOLIA][PUTATIVE]	Esterase
5560	738	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE PROTEIN KINASE GI:8777368 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5568	739	VETISPIRADIENE SYNTHASE GI:9294376 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase

5569	740	GLYCOSYL TRANSFERASE GI:7268597 FROM [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Transferases
5571	741	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1405837 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5573	742	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE KINASE GI:1405837 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5585	743	RECEPTOR SERINE/THREONINE KINASE PR5, PUTATIVE SIMILAR TO RECEPTOR SERINE/THREONINE KINASE PR5 GI:1235680 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5590	744	POTASSIUM TRANSPORTER, PUTATIVE SIMILAR TO POTASSIUM TRANSPORTER GI:2654088 FROM [ARABIDOPSIS THALIANA]	Transporter
5601	745	CARBONIC ANHYDRASE, PUTATIVE SIMILAR TO CARBONIC ANHYDRASE GI:882241 FROM [FLAVERIA LINEARIS]	Anhydrase
5605	746	PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA], IDENTICAL TO RESIDUES 1-319 OF SERINE/THREONINE KINASE-LIKE PROTEIN GB: AAC18796 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5606	747	PROTEIN KINASE SIMILAR TO C-TERMINAL REGION HAS SIMILARITY TO C-TERMINAL REGION OF PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5610	748	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE PRECURSOR (PECTINASE) GB:P35336 [ACTINIDIA CHINENSIS][PUTATIVE]	Glycosylase
5612	749	PROTEIN KINASE SIMILAR TO C-TERMINAL REGION OF S-RECEPTOR KINASES GB:BAA21132, GB:BAA06285 [BRASSICA RAPA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein

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5613	750	PROTEIN KINASE SIMILAR TO C-TERMINAL REGION OF S-RECEPTOR KINASE PRECURSOR GB:JQ1677 [BRASSICA NAPUS]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5634	751	PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5642	752	PHOSPHOGLUCOMUTASE, PUTATIVE SIMILAR TO PHOSPHOGLUCOMUTASE GI:534981 FROM [SPINACIA OLERACEA]	Mutase
5653	753	AUXIN TRANSPORT PROTEIN REH1, PUTATIVE SIMILAR TO AUXIN TRANSPORT PROTEIN REH1 GI:3377509 FROM [ORYZA SATIVA]	Transporter
5663	754	BILIRUBIN OXIDASE SIMILAR TO; SPORE COAT PROTEIN-LIKE PROTEIN SIMILAR TO SPORE COAT PROTEIN A GB:P07788 FROM [BACILLUS SUBTILIS] AND GB:Q12737 [MYROTHECIUM VERRUCARIA]	Oxidase
5666	755	GLUCOSAMINYL (N-ACETYL) TRANSFERASE GB:4758422 FROM [HOMO SAPIENS], UNKNOWN PROTEIN SIMILAR TO	Transferases
5675	756	FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE I, KETOACYL-COA SYNTHASE SIMILAR TO, GB: AAC99312[PUTATIVE]	Synthase
5676	757	DEHYDROGENASE SIMILAR TO D-THREONINE DEHYDROGENASE GB:BAA34184[PUTATIVE]	Dehydrogenases
5677	758	DEHYDROGENASE SIMILAR TO D-THREONINE DEHYDROGENASE GB:BAA34184[PUTATIVE]	Dehydrogenases
5681	759	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE SIMILAR TO UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR GB:Q09332 [DROSOPHILA MELANOGASTER][PUTATIVE]	Transferases
5684	760	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
5712	761	AMINO ACID PERMEASE SIMILAR TO AMINO ACID PERMEASE GB:AAB48944 FROM [NICOTIANA SYLVESTRIS][PUTATIVE]	Transporter

5714	762	LIPASE/HYDROLASE GDSDL-motif SIMILAR TO PUTATIVE LIPASE/HYDROLASE GDSDL-motif GB:AAC23769 AND GB:AAD12024[PUTATIVE]	Lipase
5716	763	PEROXIDASE ATP4A IDENTICAL TO GB:CAA67309 GI:1429213 FROM [ARABIDOPSIS THALIANA]	Oxidase
5723	764	HYPOXANTHINE RIBOSYL TRANSFERASE, PUTATIVE SIMILAR TO HYPOXANTHINE RIBOSYL TRANSFERASE GB:AAC46403 GI:2689037 FROM [VIBRIO PARAHAEMOLYTICUS]	Transferases
5731	765	PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GB:BAA11869 GI:1389566 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
5736	766	SUCROSE TRANSPORT PROTEIN SUC1 IDENTICAL TO GB:S38197 FROM [ARABIDOPSIS THALIANA]	Transporter
5737	767	SUCROSE TRANSPORT PROTEIN SIMILAR TO SUCROSE TRANSPORT PROTEIN SUC1 GB:S38197 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
5740	768	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE SIMILAR TO HISTIDINOL-PHOSPHATE AMINOTRANSFERASE GB:CAA70403 FROM [NICOTIANA TABACUM][PUTATIVE]	Transferases
5747	769	FUCOSYLTRANSFERASE 9 GB:NP_034373 FROM [MUS MUSCUS], HYPOTHETICAL PROTEIN PREDICTED BY GENEFINDER, CONTAINS SIMILARITY TO	Transferases
5761	770	OLIGOPEPTIDE TRANSPORTER, PUTATIVE SIMILAR TO LEOPT1 [LYCOPERSICON ESCULENTUM] GI:4102839	Transporter
5766	771	LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO GI:3641252 FROM [MALUS X DOMESTICA] (PLANT MOL. BIOL. 40 (6), 945-957 (1999))	Kinase, Protein
5767	772	PHOSPHOGLYCERATE DEHYDROGENASE, PUTATIVE CONTAINED WITHIN GI:6626247 FROM [ARCHAEOGLOBUS FULgidus]	Dehydrogenase
5777	773	LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO GI:3641252 FROM [MALUS X DOMESTICA] (PLANT MOL. BIOL. 40 (6), 945-957 (1999))	Kinase, Protein

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5793	774	RECEPTOR-LIKE PROTEIN KINASE CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (5 COPIES), PF00069 EUKARYOTIC PROTEIN DOMAIN[PUTATIVE]	Kinase, Protein
5801	775	PROTEIN KINASE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase, Protein
5815	776	CINNAMYL-ALCOHOL DEHYDROGENASE SIMILAR TO CINNAMYL-ALCOHOL DEHYDROGENASE GB: AAC35846 [MEDICAGO SATIVA][PUTATIVE]	Dehydrogenases
5817	777	P-TYPE TRANSPORTING ATPASE SIMILAR TO ATPASE II GB:AAD34706 [HOMO SAPIENS][PUTATIVE]	Transporter
5827	778	THREONINE SYNTHASE, PUTATIVE SIMILAR TO THREONINE SYNTHASE GI:4850369 FROM [ARABIDOPSIS THALIANA]	Synthase
5843	779	MANDELONITRILE LYASE GI:288115 FROM [PRUNUS SEROTINA], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Lyase
5851	780	MANDELONITRILE LYASE, PUTATIVE SIMILAR TO MANDELONITRILE LYASE GI:288115 FROM [PRUNUS SEROTINA]	Lyase
5862	781	GLYCOSYL TRANSFERASE CONTAINS PFAM PROFILE: PF00534 GLYCOSYL TRANSFERASES GROUP I[PUTATIVE]	Transferases
5880	782	STEROID 22-ALPHA-HYDROXYLASE, PUTATIVE SIMILAR TO STEROID 22-ALPHA-HYDROXYLASE GI:2935342 FROM [ARABIDOPSIS THALIANA]	Hydroxylase
5881	783	GLUCOSIDASE II BETA-SUBUNIT GI:5452942 FROM [MUS MUSCULUS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Glycosylase
5883	784	SUCROSE SYNTHASE, PUTATIVE SIMILAR TO SUCROSE SYNTHASE GI:4468151 FROM [CRATEROSTIGMA PLANTAGINEUM]	Synthase
5893	785	LYSOPHOSPHOLIPASE HOMOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE HOMOLOG GI:2801536 FROM [ORYZA SATIVA]	Lipase

5898	786	DIPHOSPHONOSITOL POLYPHOSPHATE PHOSPHOHYDROLASE GI:3978224 FROM [HOMO SAPIENS], UNKNOWN PROTEIN CONTAINS SIMILARITY TO	Hydrolase
5903	787	AUXIN TRANSPORTER SPLICE VARIANT B, PUTATIVE SIMILAR TO GI:7109715 FROM [ARABIDOPSIS THALIANA]	Transporter
5905	788	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
5918	789	UDP-N-ACETYLGLUCOSAMINE-N-ACETYLMURAMYL- (PENTAPEPTIDE)-PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE SIMILAR TO PUTATIVE UDP-N-ACETYLGLUCOSAMINE-N- ACETYLMURAMYL-(PENTAPEPTIDE)- PYROPHOSPHORYL-UNDECAPRENOL N- ACETYLGLUCOSAMINE TRANSFERASE GB:O07670 [ENTEROCOCCUS HIRAE][PUTATIVE]	Transferases
5919	790	ALPHA/BETA HYDROLASE FOLD	Hydrolase
5932	791	GLUCOSYLTRANSFERASE SIMILAR TO GLUCOSYLTRANSFERASE GB:AAB36653 FROM [NICOTIANA TABACUM][PUTATIVE]	Transferases
5935	792	LIPASE SIMILAR TO LIPASE GB:CAA74737 FROM [DROSOPHILA MELANOGASTER][PUTATIVE]	Lipase
5941	793	URIDINE KINASE GB:AAF09747 FROM [DEINOCOCCUS RADIODURANS], UNKNOWN PROTEIN CONTAINS A REGION SIMILAR TO	Kinase
5942	794	PROTEASE IV SIMILAR TO PROTEASE IV GB:AAA57008 FROM [ESCHERICHIA COLI][PUTATIVE]	Protease
5943	795	STRICTOSIDINE SYNTHASE SIMILAR TO STRICTOSIDINE SYNTHASE 3 PRECURSOR GB:P92976[PUTATIVE]	Synthase
5944	796	STRICTOSIDINE SYNTHASE SIMILAR TO STRICTOSIDINE SYNTHASE 1/2 PRECURSOR GB:P94111[PUTATIVE]	Synthase

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5945	797	STRICTOSIDINE SYNTHASE EXTREMELY SIMILAR TO STRICTOSIDINE SYNTHASE 1/2 PRECURSOR GB:P94111[PUTATIVE]	Synthase
5947	798	2-ISOPROPYLMALATE SYNTHASE SIMILAR TO 2-ISOPROPYLMALATE SYNTHASE GB: AAB61598 FROM [LYCOPERSICON PENNELLII][PUTATIVE]	Synthase
5950	799	ADENOSINE KINASE (EC 2.7.1.20) GB:S52758 FROM [LEISHMANIA DONOVANI], HYPOTHETICAL PROTEIN PREDICTED BY GENSCAN+, SIMILAR TO	Kinase
5952	800	FLAVONOL SULFOTRANSFERASE SIMILAR TO FLAVONOL 4'-SULFOTRANSFERASE GB:P52837 FROM [FLAVERIA CHLORAEFOLIA][PUTATIVE]	Transferases
5964	801	GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE SIMILAR TO GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE GB:AAF12F49 FROM [DEINOCOCCUS RADIODURANS][PUTATIVE]	Esterase
5967	802	MITOCHONDRIAL CARRIER PROTEIN SIMILAR TO GB:CAA21437 FROM [SCHIZOSACCHAROMYCES POMBE][PUTATIVE]	Transporter
5979	803	RECEPTOR PROTEIN KINASE SIMILAR TO BRASSINOSTEROID INSENSITIVE 1 GB: AAC49810 (PUTATIVE RECEPTOR PROTEIN KINASE); CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (17 REPEATS), PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
5981	804	ALPHA GALACTOSYLTRANSFERASE SIMILAR TO ALPHA GALACTOSYLTRANSFERASE GB:CAB52246 [TRIGONELLA FOENUM-GRAECUM] (PLANT CELL WALL MATRIX POLYSACCHARIDE BIOSYNTHESIS)[PUTATIVE]	Transferases
5982	805	EXONUCLEASE CONTAINS PFAM PROFILE: PF00929 EXONUCLEASE[PUTATIVE]	Nuclease
5985	806	XYLOGLUCAN FUcosylTRANSFERASE SIMILAR TO XYLOGLUCAN FUcosylTRANSFERASE GB:AAD41092 [ARABIDOPSIS THALIANA] (ENZYME INVOLVED IN PLANT CELL WALL BIOSYNTHESIS: SCIENCE 284, 1976-1979 (1999))[PUTATIVE]	Transferases

5989	807	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
5990	808	GERANYLGERANYL REDUCTASE IDENTICAL TO GERANYLGERANYL REDUCTASE GB:Y14044 [ARABIDOPSIS THALIANA] (INVOLVEMENT: CHLOROPHYLL, THE TOCOPHEROL AND THE PHYLLOQUINONE PATHWAYS EUR J BIOCHEM 1998 JAN 15;251(1-2):413-7)	Reductase
6001	809	GLUTATHIONE S-TRANSFERASE SIMILAR TO PUTATIVE GLUTATHIONE S-TRANSFERASE GB:CAA10060 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00043 GLUTATHIONE S- TRANSFERASES[PUTATIVE]	Transferases
6005	810	ALPHA/BETA HYDROLASE FOLD	Hydrolase
6012	811	ISOCHORISMATE SYNTHASE (ICSI) IDENTICAL TO ISOCHORISMATE SYNTHASE (ICSI) GB:AF078080 (CATALYZES CHORISMIC ACID TO ISOCHORISMIC ACID PLANT PHYSIOL. 118 (4), 1536 (1998))	Synthase
6013	812	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, 3' PARTIAL SIMILAR TO PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:CAA16616 [ARABIDOPSIS THALIANA][PUTATIVE]	Transferases
6049	813	DNA-3-METHYLADENINE GLYCOSYLASE I SIMILAR TO PUTATIVE DNA-3-METHYLADENINE GLYCOSYLASE I (TAG I) GB:P05100 [ESCHERICHIA COLI][PUTATIVE]	Glycosylase
6063	814	3-METHYLADENINE DNA GLYCOSYLASE, PUTATIVE SIMILAR TO GI:1669515 FROM [SCHIZOSACCHAROMYCES POMBE] (GENE 177 (1-2), 229-235 (1996))	Glycosylase
6067	815	GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE 1, PUTATIVE SIMILAR TO GI:6939839 FROM [ORYZA SATIVA]	Reductase
6068	816	NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995))	Reductase

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6069	817	NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995))	Reductase
6070	818	NADPH OXIDOREDUCTASE, PUTATIVE SIMILAR TO GI:1708420 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 270 (44), 26224-26231 (1995))	Reductase
6084	819	CYTOKININ OXIDASE, PUTATIVE SIMILAR TO GB:CAA77151 FROM [ZEA MAYS] (PLANT J. 17 (6), 615- 626 (1999))	Oxidase
6085	820	PROTEASE, PUTATIVE SIMILAR TO SP:P36774 FROM [MYXOCOCCUS XANTHUS]	Protease
6101	821	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE RECEPTOR-LIKE PROTEIN KINASE GB:AAB36558 GI:1684913 FROM [IPOMOEA NIL]	Kinase, Protein
6114	822	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:CAB08077 GI:1944575 FROM [LYCOPERSICON ESCULENTUM]	Esterase
6117	823	RECEPTOR KINASE (CLV1) IDENTICAL TO RECEPTOR KINASE (CLV1) GB:AAB58929 GI:2160756 [ARABIDOPSIS THALIANA]	Kinase, Protein
6139	824	RNA PSEUDOURIDYLATE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF00849 RNA PSEUDOURIDYLATE SYNTHASE	Synthase
6143	825	S-ADENOSYL-METHIONINE-STEROL-C- METHYLTRANSFERASE, PUTATIVE ALMOST IDENTICAL TO S-ADENOSYL-METHIONINE-STEROL-C- METHYLTRANSFERASE GI:2246456 FROM [ARABIDOPSIS THALIANA]	Transferases
6146	826	PSEUDOURIDYLATE SYNTHASE 2 GI:1403092 FROM [SACCHAROMYCES CEREVISIAE][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Synthase
6147	827	ALPHA-AMYLASE, PUTATIVE SIMILAR TO ALPHA- AMYLASE GI:7532799 FROM [MALUS DOMESTICA]	Glycosylase
6150	828	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GI:1944574 FROM [LYCOPERSICON ESCUENTUM]	Esterase

6170	829	PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A); CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
6176	830	PHOSPHATE TRANSPORTER SIMILAR TO PHOSPHATE TRANSPORTER GB:BAA20522 [CATHARANTHUS ROSEUS][PUTATIVE]	Transporter
6180	831	CINNAMOYL-COA REDUCTASE SIMILAR TO CINNAMOYL-COA REDUCTASE GB:CAA56103 [EUCALYPTUS GUNNII][PUTATIVE]	Reductase
6188	832	PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT SIMILAR TO PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT GB:AAD30596 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase
6201	833	12-OXOPHYTODIENOATE REDUCTASE (OPR1) IDENTICAL TO 12-OXOPHYTODIENOATE REDUCTASE OPR1 GB: AAC78440 [ARABIDOPSIS THALIANA]	Reductase
6202	834	12-OXOPHYTODIENOATE REDUCTASE (OPR2) IDENTICAL TO 12-OXOPHYTODIENOATE REDUCTASE OPR2 GB: AAC78441 [ARABIDOPSIS THALIANA]	Reductase
6212	835	CATECHOL O-METHYLTRANSFERASE SIMILAR TO CATECHOL O-METHYLTRANSFERASE GB:CAA55358 [VANILLA PLANIFOLIA][PUTATIVE]	Transferases
6232	836	URIDYL TRANSFERASE GI:4406764 FROM [ARABIDOPSIS THALIANA]DEACETYL VINDOLINE 4-O-ACETYLTRANSFERASE, GB: AAC9931; UNKNOWN PROTEIN SIMILAR TO UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Transferases
6238	837	CARBOXYPHOSPHONOENOLPYRUVATE MUTASE, PUTATIVE SIMILAR TO CARBOXYPHOSPHONOENOLPYRUVATE MUTASE GI:47149 FROM [STREPTOMYCES HYGROSCOPICUS]	Mutase
6242	838	PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GI:1161565 FROM [LYCOPERSICON ESCULENTUM]	Oxidase
6243	839	AUXIN TRANSPORT PROTEIN EIR1, PUTATIVE SIMILAR TO AUXIN TRANSPORT PROTEIN EIR1 GI:3377507 FROM [ARABIDOPSIS THALIANA]	Transporter

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6259	840	RECEPTOR-LIKE PROTEIN KINASE GI:7529754 FROM [ARABIDOPSIS THALIANA][HYPOTHÉTICAL PROTEIN SIMILAR TO]	Kinase, Protein
6264	841	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE, PUTATIVE SIMILAR TO 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE GI:3386565 FROM [SORGHUM BICOLOR]	Oxidase
6269	842	AMINO ACID CARRIER, PUTATIVE SIMILAR TO AMINO ACID CARRIER GI:3293031 FROM [RICINUS COMMUNIS]	Transporter
6274	843	LYSOPHOSPHOLIPASE ISOLOG, PUTATIVE SIMILAR TO LYSOPHOSPHOLIPASE ISOLOG GI:1931639 FROM [ARABIDOPSIS THALIANA]	Lipase
6279	844	ASPARTIC PROTEASE, NUCELLIN-LIKE PROTEIN SIMILAR TO NUCELLIN GB:AAB96882 [HORDEUM VULGARE] (NUCELLIN: SIMILAR TO ASPARTIC PROTEASE AND ITS SPECIFIC EXPRESSION IN NUCELLAR CELLS DURING DEGENERATION)	Protease
6280	845	ASCORBATE PEROXIDASE IDENTICAL TO THYLAKOID-BOUND ASCORBATE PEROXIDASE GB:CAA67426 [ARABIDOPSIS THALIANA] THYLAKOID-BOUND	Oxidase
6283	846	CAFFEIC ACID 3-O-METHYLTRANSFERASE SIMILAR TO CAFFEIC ACID 3-O-METHYLTRANSFERASE GB:O23760 [CLARKIA BREWERI][PUTATIVE]	Transferases
6284	847	CAFFEIC ACID 3-O-METHYLTRANSFERASE SIMILAR TO CAFFEIC ACID 3-O-METHYLTRANSFERASE GB:O23760 [CLARKIA BREWERI][PUTATIVE]	Transferases
6299	848	AUX1-LIKE PERMEASE SIMILAR TO AUX1 (REGULATOR OF ROOT GRAVITROPISM, PUTATIVE PERMEASE) GB:CAA67308 [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
6308	849	ENDO-1,3-BETA-GLUCANASE SIMILAR TO ENDO-1,3-BETA-GLUCANASE GB:BAA21110 [GOSSYPIUM HIRSUTUM][PUTATIVE]	Glycosylase
6309	850	ENDO-1,3-BETA-GLUCANASE SIMILAR TO ENDO-1,3-BETA-GLUCANASE GB:BAA21110 [GOSSYPIUM HIRSUTUM][PUTATIVE]	Glycosylase

6312	851	REVERSE TRANSCRIPTASE GI:976278 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transcriptase
6321	852	NADH DEHYDROGENASE SUBUNIT 1[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Dehydrogenase
6335	853	PHOSPHOGLYCERATE MUTASE, PUTATIVE SIMILAR TO PHOSPHOGLYCERATE MUTASE GI:8979237 FROM [CHLAMYDIA MURIDARUM]	Mutase
6336	854	XYLOSIDASE, PUTATIVE SIMILAR TO XYLOSIDASE GI:2102655 FROM [ASPERGILLUS NIGER]	Glycosylase
6339	855	TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPB) IDENTICAL TO TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPB) GB:AF007779 [ARABIDOPSIS THALIANA] (TREHALOSE SYNTHESIS, A COMMON DISACCHARIDE THAT APPEARS TO PLAY A MAJOR ROLE IN DESICCATION TOLERANCE, PLANT J 1998 MAR;13(5):673-83)	Phosphatase
6344	856	TRANSPORTER CONTAINS PFAM PROFILE: PF00083 SUGAR (AND OTHER) TRANSPORTER[PUTATIVE]	Transporter
6351	857	PROTEIN PHOSPHATASE 2C SIMILAR TO PROTEIN PHOSPHATASE 2C GB:CAA72341 [MEDICAGO SATIVA]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C[PUTATIVE]	Phosphatase
6355	858	METHYLTRANSFERASE GB:AAD17428 [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN, 5' PARTIAL SIMILAR TO PUTATIVE	Transferases
6357	859	UDP-GLUCOSE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GI:3928543 FROM [ARABIDOPSIS THALIANA]	Transferases
6362	860	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA]	Transferases
6363	861	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA]	Transferases

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6364	862	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA]	Transferases
6365	863	GLUTATHIONE S-TRANSFERASE, PUTATIVE SIMILAR TO 2,4-D INDUCIBLE GLUTATHIONE S-TRANSFERASE GI:2920666 FROM [GLYCINE MAX]	Transferases
6366	864	GLUTATHIONE TRANSFERASE, PUTATIVE SIMILAR TO GLUTATHIONE TRANSFERASE GI:2853219 FROM [CARICA PAPAYA]	Transferases
6368	865	EXOPOLYGALACTURONASE, PUTATIVE SIMILAR TO EXOPOLYGALACTURONASE GI:311962 FROM [ARABIDOPSIS THALIANA]	Glycosylase
6372	866	GIBBERELLIN 2- OXIDASE IDENTICAL TO GIBBERELLIN 2- OXIDASE GI:4678366 FROM [ARABIDOPSIS THALIANA]	Oxidase
6376	867	BETA-AMYRIN SYNTHASE, PUTATIVE SIMILAR TO BETA-AMYRIN SYNTHASE GI:3688600 FROM [PANAX GINSENG]	Synthase
6380	868	BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT GI:2281103 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Glycosylase
6381	869	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:9280288 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6383	870	FLAVANONE 3-HYDROXYLASE, PUTATIVE SIMILAR TO FLAVANONE 3-HYDROXYLASE GI:727410 FROM [PERSEA AMERICANA]	Hydroxylase
6420	871	INORGANIC PYROPHOSPHATASE IDENTICAL TO VACUOLAR-TYPE H ⁺ -TRANSLOCATING INORGANIC PYROPHOSPHATASE GI:6901678 FROM [ARABIDOPSIS THALIANA]	Phosphatase
6426	872	LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 2 GI:3360291 FROM [ZEA MAYS]	Kinase, Protein

6465	873	NA+/H ⁺ ANTIPORTER GI:4558666 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transporter
6471	874	ENT-KAURENE SYNTHASE, PUTATIVE SIMILAR TO ENT-KAURENE SYNTHASE GI:3056725 FROM [ARABIDOPSIS THALIANA]	Synthase
6473	875	BETA-1,3-GLUCANASE-LIKE PROTEIN GI:9758115 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Glycosylase
6475	876	2-DEHYDRO-3-DEOXYPHOSPHOOCTONATE ALDOLASE, PUTATIVE SIMILAR TO 2-DEHYDRO-3-DEOXYPHOSPHOOCTONATE ALDOLASE GI:1683630 FROM [MANNHEIMIA HAEMOLYTICA]	Aldolase
6486	877	NA+/H ⁺ ANTIPORTER GI:1655701 FROM [XENOPUS LAEVIS][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transporter
6487	878	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6488	879	PROTEIN PHOSPHATASE-2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GI:3643088 FROM [MESEMBRYANTHEMUM CRYSTALLINUM]	Phosphatase
6492	880	WALL-ASSOCIATED KINASE 4, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 4 GI:3355308 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6493	881	WALL-ASSOCIATED KINASE 2, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 2 GI:4826399 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6532	882	RECEPTOR PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR PROTEIN KINASE GI:1389566 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6538	883	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:7381227 FROM [LYCOPERSICON ESCULENTUM]	Glycosylase
6541	884	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE GI:7381227 FROM [LYCOPERSICON ESCULENTUM]	Glycosylase

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6551	885	ALPHA/BETA HYDROLASE FOLD	Hydrolase
6554	886	SULFATE TRANSPORTER CONTAINS PFAM PROFILE: PF00916 SULFATE TRANSPORTER FAMILY[PUTATIVE]	Transporter
6555	887	IRON/ASCORBATE OXIDOREDUCTASE FAMILY[PUTATIVE]	Reductase
6556	888	GIBBERELLIN 3 BETA-HYDROXYLASE SIMILAR TO GIBBERELLIN 3 BETA-HYDROXYLASE GB: AAC83647 [ARABIDOPSIS THALIANA][PUTATIVE]	Hydroxylase
6557	889	GIBBERELLIN 3 BETA-HYDROXYLASE IDENTICAL TO GIBBERELLIN 3 BETA-HYDROXYLASE GB: AAC83647 [ARABIDOPSIS THALIANA]	Hydroxylase
6559	890	ASPARTATE AMINOTRANSFERASE SIMILAR TO ASPARTATE AMINOTRANSFERASE B GB: Q06191 [SINORHIZOBIUM MELiloti][PUTATIVE]	Transferases
6573	891	AMINO ACID TRANSPORTER PROTEIN DOMAIN	Transporter
6586	892	PROTEIN KINASE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE I GB: AAC27894 FROM [ZEA MAYS][PUTATIVE]	Kinase, Protein
6604	893	CINNAMOYL COA REDUCTASE, PUTATIVE SIMILAR TO CINNAMOYL COA REDUCTASE GB: AAF43141 GI: 7239228 FROM [POPULUS TREMULOIDES]	Reductase
6609	894	PROTEIN KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI: 2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
6633	895	AMINO ACID PERMEASE IDENTICAL TO GP: AF019637[PUTATIVE]	Transporter
6658	896	AUXIN TRANSPORT PROTEIN IDENTICAL TO GP: J3785972 AC005560[PUTATIVE]	Transporter
6663	897	PROTEIN TRANSPORT PROTEIN SEC12P IDENTICAL TO GB: M95796, CONTAINS A WD-40 REPEAT DOMAIN[PUTATIVE]	Transporter
6679	898	BETA-1,3-GLUCANASE [PUTATIVE]	Glycosylase
6699	899	HISTIDINE KINASE [PUTATIVE]	Kinase, Protein
6701	900	XYLOGLUCAN-SPECIFIC GLUCANASE IDENTICAL TO GB: D63509[PUTATIVE]	Glycosylase

6704	901	PURPLE ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE]	Esterase
6705	902	PURPLE ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE]	Esterase
6711	903	RECEPTOR PROTEIN KINASE SIMILAR TO BRASSINOSTEROID INSENSITIVE PROTEIN[PUTATIVE]	Kinase, Protein
6714	904	NA+/H+ ANTIPORTER [PUTATIVE]	Transporter
6716	905	GLUTAMATE DECARBOXYLASE [PUTATIVE]	Decarboxylase
6717	906	GLUTAMATE DECARBOXYLASE [PUTATIVE]	Decarboxylase
6737	907	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
6752	908	CINNAMOYL-COA REDUCTASE [PUTATIVE]	Reductase
6759	909	DNA POLYMERASE III GAMMA SUBUNIT [SIMILAR TO]	Polymerase
6763	910	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
6770	911	TRANSPORT PROTEIN [PUTATIVE]	Transporter
6775	912	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
6781	913	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
6782	914	PECTATE LYASE [PUTATIVE]	Lyase
6788	915	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
6801	916	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
6806	917	RIBONUCLEASE, RNS1 IDENTICAL TO GB:U05206; CONTAINS A RIBONUCLEASE T2 FAMILY HISTIDINE ACTIVE SITE SIGNATURE (PDOC00459)[PUTATIVE]	Nuclease
6844	918	HORMONE-RECEPTOR DOMAIN (PROSITE: QDOC50227)	Receptor
6860	919	ESTERASE (CONTAINS AN ESTERASE/LIPASE/THIOESTERASE ACTIVE SITE SERINE DOMAIN (PROSITE: PS50187); RELATED TO PLANT SENSITIVE RESPONSE PROTEINS[PUTATIVE])	Esterase
6875	920	URIDYLYL TRANSFERASE [PUTATIVE]	Transferases
6877	921	STEROID SULFOTRANSFERASE [PUTATIVE]	Transferases
6878	922	STEROID SULFOTRANSFERASE [PUTATIVE]	Transferases

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6890	923	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
6892	924	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
6894	925	IRON TRANSPORTER ROOT [PUTATIVE]	Transporter
6908	926	RIBONUCLEASE E [PUTATIVE]	Nuclease
6910	927	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
6920	928	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE [PUTATIVE]	Synthase
6922	929	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
6933	930	PROTEIN PHOSPHATASE [PUTATIVE]	Phosphatase
6935	931	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
6936	932	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
6946	933	FERREDOXIN-THIOREDOXIN REDUCTASE [PUTATIVE]	Reductase
6952	934	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
6980	935	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
6986	936	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE [PUTATIVE]	Carboxylase
7023	937	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7038	938	BETA-1,3-GLUCANASE [PUTATIVE]	Glycosylase
7050	939	SERINE PROTEASE [PUTATIVE]	Protease
7057	940	ENOYL-ACP REDUCTASE (ENR-A) IDENTICAL TO GB:Y13860	Reductase
7063	941	12-OXOPHYTODIENOATE-10,11-REDUCTASE	Reductase
7110	942	ENDOXYLOGLUCAN GLYCOSYLTRANSFERASE IDENTICAL TO GB:D16454[PUTATIVE]	Transferases
7115	943	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE	Oxidase
7123	944	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein

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7125	945	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7126	946	GAG-PROTEASE POLYPROTEIN POSSIBLE 3' PARTIAL[PUTATIVE]	Protease
7133	947	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE.(PDQC00100)[PUTATIVE]	Kinase, Protein
7168	948	ABC TRANSPORTER [PUTATIVE]	Transporter
7262	949	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE [PUTATIVE]	Synthase
7263	950	REVERSE TRANSCRIPTASE TA1-1; GB:AAD17398[HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase
7295	951	C-1-TETRAHYDROFOLATE SYNTHASE [PUTATIVE]	Synthase
7331	952	N-ACETYLGLUCOSAMINYLTRANSFERASE [PUTATIVE]	Transferases
7352	953	NA/H ANTIPORTER [PUTATIVE]	Transporter
7365	954	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7366	955	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7367	956	ASPARTATE AMINOTRANSFERASE [PUTATIVE]	Transferases
7403	957	PROLINE IMINOPEPTIDASE IDENTICAL TO GP:1710151:U72711	Protease
7404	958	PROTEIN PHOSPHATASE 2C [PUTATIVE]	Phosphatase
7436	959	ENDOXYLOGLUCAN GLYCOSYLTRANSFERASE [PUTATIVE]	Transferases
7441	960	SUCROSE-PROTON SYMPORTER. [PUTATIVE]	Transporter
7443	961	1,4-BETA-XYLAN ENDOHYDROLASE	Hydrolase
7446	962	VACUOLAR SORTING RECEPTOR-LIKE PROTEIN	Receptor
7448	963	VACUOLAR SORTING RECEPTOR-LIKE PROTEIN	Receptor
7465	964	STEROID SULFOTRANSFERASE [PUTATIVE]	Transferases
7500	965	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7504	966	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7509	967	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase

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7516	968	POLYGALACTURONASE [PUTATIVE]	Glycosylase
7517	969	POLYGALACTURONASE [PUTATIVE]	Glycosylase
7518	970	POLYGALACTURONASE [PUTATIVE]	Glycosylase
7519	971	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
7520	972	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
7522	973	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7533	974	FERREDOXIN-NITRITE REDUCTASE	Reductase
7543	975	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7546	976	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7550	977	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYCLOPHILIN-TYPE [PUTATIVE]	Isomerase
7577	978	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7588	979	BETA-1,3-ENDOGLUCANASE, 5' PARTIAL [PUTATIVE]	Glycosylase
7589	980	LRR RECEPTOR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7592	981	BETA-KETOACYL-COA SYNTHASE [PUTATIVE]	Synthase
7604	982	PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE]	Phosphatase
7612	983	ARGININE DECARBOXYLASE IDENTICAL TO GP:1590814:U52851	Decarboxylase
7623	984	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7636	985	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7640	986	GLUCONOKINASE [PUTATIVE]	Kinase
7651	987	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
7659	988	TETRACYCLINE TRANSPORTER PROTEIN [PUTATIVE]	Transporter
7660	989	TETRACYCLINE TRANSPORTER PROTEIN [PUTATIVE]	Transporter
7661	990	TETRACYCLINE TRANSPORTER-LIKE PROTEIN, 3' PARTIAL IDENTICAL TO EGAD 110957 119053	Transporter
7664	991	PROTEIN KINASE DOMAIN	Kinase, Protein

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7685	992	POLY(A) POLYMERASE [PUTATIVE]	Polymerase
7688	993	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7691	994	SERINE ACETYLTRANSFERASE (GB:AF112303)	Transferases
7708	995	SERINE PEPTIDASE RELATED TO THYMUS-SPECIFIC FROM HOMO SAPIENS	Protease
7714	996	PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE]	Phosphatase
7715	997	PEROXIDASE [PUTATIVE]	Oxidase
7716	998	PEROXIDASE [PUTATIVE]	Oxidase
7720	999	AAA-TYPE ATPASE [PUTATIVE]	ATPase
7724	1000	INORGANIC PYROPHOSPHATASE [PUTATIVE]	Phosphatase
7746	1001	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7752	1002	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7755	1003	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
7756	1004	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
7761	1005	GERANYLGERANYL PYROPHOSPHATE SYNTHASE [PUTATIVE]	Synthase
7763	1006	GERANYLGERANYL PYROPHOSPHATE SYNTHASE CONTAINS GB:L22347[PUTATIVE]	Synthase
7779	1007	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE [PUTATIVE]	Glycosylase
7789	1008	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7798	1009	PEROXIDASE (ATP22A) IDENTICAL TO GB:Y08781	Oxidase
7801	1010	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
7805	1011	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
7806	1012	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase

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7807	1013	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE]	N-Transferases
7810	1014	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
7813	1015	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7815	1016	PECTINESTERASE [PUTATIVE]	Esterase
7817	1017	SERINE PROTEASE [PUTATIVE]	Protease
7819	1018	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7821	1019	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
7823	1020	PROTEIN KINASE, 5'PARTIAL [PUTATIVE]	Kinase, Protein
7844	1021	BETA-1,3-ENDOGLUCANASE [PUTATIVE]	Glycosylase
7850	1022	CYTOKININ OXIDASE [PUTATIVE]	Oxidase
7855	1023	ALPHA/BETA HYDROLASE FOLD (PF00561).[PUTATIVE]; ESTERASE CONTAINS ESTERASE/LIPASE/THIOESTERASE ACTIVE SITE SERINE (PS50187)	Hydrolase
7857	1024	CYTIDINE DEAMINASE [PUTATIVE]	Deaminase
7859	1025	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE	Oxidase
7860	1026	POTASSIUM/PROTON ANTIPORTER [PUTATIVE]	Transporter
7894	1027	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE [PUTATIVE]	Reductase
7905	1028	PROTEIN PHOSPHATASE 2C [PUTATIVE]	Phosphatase
7930	1029	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
7962	1030	PROTEIN PHOSPHATASE 2C [PUTATIVE]	Phosphatase
7969	1031	(1-4)-BETA-MANNAN ENDOHYDROLASE	Hydrolase
7970	1032	RIBOFLAVIN SYNTHASE ALPHA CHAIN [PUTATIVE]	Synthase
7985	1033	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN [PUTATIVE]	Transporter
7986	1034	LRR RECEPTOR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8002	1035	MAJOR INTRINSIC (CHANNEL) PROTEIN [PUTATIVE]	Channel
8005	1036	AUX1-LIKE AMINO ACID PERMEASE	Transporter

8016	1037	SIGNAL SEQUENCE RECEPTOR, ALPHA SUBUNIT (SSR-ALPHA) SAME AS GP: 1174448[PUTATIVE]	Receptor
8036	1038	XYLULOSE KINASE [PUTATIVE]	Kinase
8047	1039	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8054	1040	DIHYDROFOLATE REDUCTASE, 3' PARTIAL [PUTATIVE]	Reductase
8059	1041	PECTINESTERASE [PUTATIVE]	Esterase
8072	1042	CELLULOSE SYNTHASE CATALYTIC SUBUNIT [PUTATIVE]	Synthase
8084	1043	CINNAMYL-ALCOHOL DEHYDROGENASE [PUTATIVE]	Dehydrogenases
8089	1044	SHIKIMATE KINASE PRECURSOR [PUTATIVE]	Kinase
8113	1045	TREHALOSE-6-PHOSPHATE PHOSPHATASE [PUTATIVE]	Phosphatase
8115	1046	BETA-HYDROXYACYL-ACP DEHYDRATASE [PUTATIVE]	Dehydratase
8131	1047	PEROXIDASE [PUTATIVE]	Oxidase
8133	1048	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
8134	1049	GTP CYCLOHYDROLASE [PUTATIVE]	Hydrolase
8137	1050	PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE 1-PHOSPHOTRANSFERASE [PUTATIVE]	Transferases
8147	1051	ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, 3' PARTIAL	Transferases
8153	1052	D-AMINO ACID DEHYDROGENASE [PUTATIVE]	Dehydrogenases
8179	1053	AMINO ACID ACETYLTRANSFERASE [PUTATIVE]	Transferases
8181	1054	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8184	1055	SERINE CARBOXYPEPTIDASE I, PSEUDOGENE SIMILAR TO SERINE CARBOXYPEPTIDASE I[PUTATIVE]	Protease
8207	1056	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8208	1057	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8210	1058	VETISPIRADIENE SYNTHASE [PUTATIVE]	Synthase

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8212	1059	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8213	1060	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8217	1061	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8232	1062	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8238	1063	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE]	N-Transferases
8241	1064	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
8242	1065	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8243	1066	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8244	1067	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8245	1068	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8246	1069	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8247	1070	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8248	1071	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8249	1072	ACETONE-CYANOHYDRIN LYASE [PUTATIVE]	Lyase
8250	1073	PECTINESTERASE [PUTATIVE]	Esterase
8263	1074	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8266	1075	GERANYLGERANYL PYROPHOSPHATE SYNTHASE IDENTICAL TO GB:U44876; SEQUENCE DISAGREES AT N-TERMINUS, SEQUENCE SUBMITTED HAS BEEN CONFIRMED FROM THREE ELECTROPHEROGRAMS.	Synthase
8274	1076	POLYGALACTURONASE [PUTATIVE]	Glycosylase
8275	1077	CINNAMOYL COA REDUCTASE [PUTATIVE]	Reductase
8279	1078	LRR RECEPTOR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8282	1079	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL	Channel
8296	1080	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8304	1081	LIMONENE CYCLASE [PUTATIVE]	Cyclase
8334	1082	H ⁺ ATPASE, PLASMA MEMBRANE, 3' PARTIAL [PUTATIVE]	ATPase

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8338	1083	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
8343	1084	CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8345	1085	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8353	1086	LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8354	1087	LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8358	1088	PEROXIDASE [PUTATIVE]	Oxidase
8399	1089	PROTEIN KINASE DOMAIN	Kinase, Protein
8420	1090	DIOXYGENASE [PUTATIVE]	Oxygenases
8429	1091	CELLULOSE SYNTHASE CATALYTIC SUBUNIT [PUTATIVE]	Synthase
8455	1092	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8498	1093	BETA-KETOACYL-COA SYNTHASE (FIDDLEHEAD) IDENTICAL TO GB:AJ010713; CONTAINS A CHALCONE AND STILBENE SYNTHASE ACTIVE SITE (PF00195)	Synthase
8502	1094	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8506	1095	RECEPTOR-LIKE PROTEIN KINASE, ERECTA IDENTICAL TO GB:U47029 AND GB:D83257; CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100); CONTAINS LRR LEUCINE RICH REPEAT DOMAINS[PUTATIVE]	Kinase, Protein
8509	1096	MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE]	Transporter
8517	1097	PECTINESTERASE [PUTATIVE]	Esterase
8518	1098	PECTINESTERASE [PUTATIVE]	Esterase
8521	1099	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8526	1100	PEROMONE RECEPTOR AR781, SIMILAR TO YEAST; IDENTICAL TO GB:D88743, CORRECTED A FRAMESHIFT FOUND IN THE ORIGINAL RECORD (AT 69530 BP), SEQUENCE SUBMITTED HAS BEEN VERIFIED FROM 10 SEQUENCE ELECTROPHEROGRAMS. THE TRANSLATION NOW STARTS FROM AN UPSTREAM ATG.	Receptor

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8528	1101	HEME OXYGENASE 2 (HO2)	Oxygenases
8533	1102	BETA-1,3-GLUCANASE [PUTATIVE]	Glycosylase
8535	1103	POLYGALACTURONASE [PUTATIVE]	Glycosylase
8537	1104	BETA-KETOACYL-COA SYNTHASE [PUTATIVE]	Synthase
8540	1105	HEME OXYGENASE 1 (HO1) IDENTICAL TO GB:AF132475; ANNOTATION UPDATED PER SETH J. DAVIS AT UNIVERSITY OF WISCONSIN-MADISON	Oxygenases
8546	1106	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8560	1107	PHOSPHOLIPASE C [PUTATIVE]	Lipase
8563	1108	BILE ACID TRANSPORTER, NA+ DEPENDENT ILEAL [PUTATIVE]	Transporter
8579	1109	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8609	1110	LIPASE [PUTATIVE]	Lipase
8611	1111	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
8624	1112	BETA-1,3-GLUCANASE [PUTATIVE]	Glycosylase
8630	1113	FLAVONOL SULFOTRANSFERASE [PUTATIVE]	Transferases
8655	1114	PREPHENATE DEHYDRATASE/CHORISMATE MUTASE [PUTATIVE]	Dehydratase
8658	1115	DTDP-GLUCOSE 4-6-DEHYDRATASE [PUTATIVE]	Dehydratase
8659	1116	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
8680	1117	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8693	1118	CARBONIC ANHYDRASE [PUTATIVE]	Anhydrase
8697	1119	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8698	1120	CYCLIC NUCLEOTIDE AND CALMODULIN- REGULATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8719	1121	PEROMONE RECEPTOR DEFICIENT MUTANT [SIMILAR TO]	Receptor
8758	1122	PARA-AMINOBENZOATE SYNTHASE AND GLUTAMINE AMIDOTRANSFERASE, A BIFUNCTIONAL ENZYME [PUTATIVE]	Synthase
8760	1123	MEMBRANE CHANNEL PROTEIN [PUTATIVE]	Channel

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8769	1124	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
8778	1125	LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8779	1126	LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8780	1127	LIGAND-GATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
8784	1128	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8789	1129	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8792	1130	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8793	1131	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8794	1132	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8800	1133	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8801	1134	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8803	1135	PROTEIN PHOSPHATASE 2C [PUTATIVE]	Phosphatase
8807	1136	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8809	1137	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8810	1138	GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:X89216	Transferases
8811	1139	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8812	1140	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8813	1141	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8814	1142	GLUTATHIONE S-TRANSFERASE [PUTATIVE]	Transferases
8834	1143	ANTHRANILATE SYNTHASE, ALPHA SUBUNIT IDENTICAL TO GB:M92354	Synthase
8836	1144	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8837	1145	MONOOXYGENASE [PUTATIVE]	Oxygenases
8838	1146	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8839	1147	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8840	1148	FLAVONOL 3-O-GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases

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8864	1149	NADH DEHYDROGENASE (UBIQUINONE OXIDOREDUCTASE) [PUTATIVE]	Dehydrogenase
8872	1150	HIGH-AFFINITY POTASSIUM TRANSPORTER (ATKUP1) IDENTICAL TO GB:AF029876	Transporter
8873	1151	FE(II) TRANSPORT PROTEIN [PUTATIVE]	Transporter
8879	1152	GLUCOSYLTRANSFERASE-[PUTATIVE]	Transferases
8880	1153	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
8885	1154	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
8887	1155	NA/H ANTIPORTER [PUTATIVE]	Transporter
8892	1156	VACUOLAR SORTING RECEPTOR [PUTATIVE]	Receptor
8894	1157	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
8895	1158	PSEUDOURIDINE SYNTHASE [PUTATIVE]	Synthase
8907	1159	SIGNAL PEPTIDASE I [PUTATIVE]	Protease
8917	1160	LIPASE [PUTATIVE]	Lipase
8929	1161	TROPINONE REDUCTASE [PUTATIVE]	Reductase
8935	1162	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8936	1163	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8945	1164	DIOXYGENASE [PUTATIVE]	Oxygenases
8946	1165	DIOXYGENASE [PUTATIVE]	Oxygenases
8947	1166	GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:Y12295	Transferases
8948	1167	GLUTATHIONE S-TRANSFERASE IDENTICAL TO GB:D17673	Transferases
8955	1168	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
8972	1169	LIPASE [PUTATIVE]	Lipase
8987	1170	GLUTAMYL TRNA REDUCTASE [PUTATIVE]	Reductase
8998	1171	DELTA 9 DESATURASE ALMOST IDENTICAL (4 AA DIFFT) TO GP:2970036	Desaturases
9001	1172	FRUCTOKINASE [PUTATIVE]	Kinase

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9016	1173	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
9017	1174	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
9031	1175	TRIACYLGLYCEROL LIPASE [PUTATIVE]	Lipase
9038	1176	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
9042	1177	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
9043	1178	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9044	1179	ACETOLACTATE SYNTHASE [PUTATIVE]	Synthase
9054	1180	NA+/H+ ANTIPORTER [PUTATIVE]	Transporter
9060	1181	GLUCAN SYNTHASE [PUTATIVE]	Synthase
9066	1182	ALANINE ACETYL TRANSFERASE [PUTATIVE]	Transferases
9067	1183	ALANINE ACETYL TRANSFERASE [PUTATIVE]	Transferases
9078	1184	HYDROLASE [PUTATIVE]	Hydrolase
9090	1185	FE(II) TRANSPORTER IDENTICAL TO GB:AF033537[PUTATIVE]	Transporter
9092	1186	BETA-AMYLASE [PUTATIVE]	Glycosylase
9108	1187	O-GLCNAC TRANSFERASE [PUTATIVE]	Transferases
9116	1188	CELLULOSE SYNTHASE [PUTATIVE]	Synthase
9117	1189	CELLULOSE SYNTHASE [PUTATIVE]	Synthase
9124	1190	CELLULOSE SYNTHASE [PUTATIVE]	Synthase
9125	1191	CELLULOSE SYNTHASE [PUTATIVE]	Synthase
9140	1192	PURPLE ACID PHOSPHATASE PRECURSOR [PUTATIVE]	Phosphatase
9143	1193	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9146	1194	PHOSPHATE TRANSPORTER [PUTATIVE]	Transporter
9173	1195	CELLULOSE SYNTHASE [PUTATIVE]	Synthase
9178	1196	POLYGALACTURONASE [PUTATIVE]	Glycosylase
9179	1197	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
9185	1198	FLAVIN-CONTAINING MONOOXYGENASE [PUTATIVE]	Oxygenases
9188	1199	TYROSINE-SPECIFIC TRANSPORT PROTEIN [PUTATIVE]	Transporter

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9220	1200	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9221	1201	CINNAMOYL-COA REDUCTASE HIGHLY SIMILAR TO F4P9.37[PUTATIVE]	Reductase
9222	1202	CINNAMOYL-COA REDUCTASE HIGHLY SIMILAR TO F4P9.36[PUTATIVE]	Reductase
9242	1203	MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE]	Transporter
9257	1204	PEROXIDASE [PUTATIVE]	Oxidase
9280	1205	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9283	1206	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
9306	1207	GIBBERELLIN 2-OXIDASE [PUTATIVE]	Oxidase
9325	1208	PROTEIN PHOSPHATASE 2C [PUTATIVE]	Phosphatase
9344	1209	VACUOLAR SORTING RECEPTOR [PUTATIVE]	Receptor
9347	1210	PHOSPHATIDYLINOSITOL-GLYCAN SYNTHASE [PUTATIVE]	Synthase
9355	1211	POTASSIUM TRANSPORTER [PUTATIVE]	Transporter
9385	1212	PEROXIDASE [PUTATIVE]	Oxidase
9409	1213	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
9412	1214	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
9413	1215	MONOOXYGENASE [PUTATIVE]	Oxygenases
9428	1216	MITOCHONDRIAL CARRIER PROTEIN [PUTATIVE]	Transporter
9469	1217	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE IDENTICAL TO AB006139	Isomerase
9500	1218	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
9502	1219	PROLINE TRANSPORTER [PUTATIVE]	Transporter
9509	1220	ASPARTYL PROTEASE FAMILY (PF00026)[PUTATIVE]	Protease
9511	1221	GIBBERELLIN BETA-HYDROXYLASE CONTAINS SIMILARITIES TO GA BETA-20-HYDROXYLASE FROM TOBACCO (GB:3327245) AND TO ETHYLENE FORMING ENZYME FROM PICEA GLAUCA (GB:L42466)[PUTATIVE]	Hydroxylase

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9512	1222	PECTINESTERASE [PUTATIVE]	Esterase
9513	1223	PECTINESTERASE [PUTATIVE]	Esterase
9517	1224	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
9518	1225	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
9519	1226	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
9520	1227	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
9521	1228	GLUCOSYL TRANSFERASE AN EST MATCHING THE 5' END OF THIS GENE (GB:AA605508) WAS ORIGINALLY DESCRIBED AS POLYADENYLATED (GB:AA006321) AND IS PROBABLY TRANSCRIBED FROM THE OPPOSITE STRAND[PUTATIVE]	Transferases
9522	1229	GLUCOSYL TRANSFERASE [PUTATIVE]	Transferases
9527	1230	GLUCAN SYNTHASE [PUTATIVE]	Synthase
9528	1231	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE [PUTATIVE]	Glycosylase
9538	1232	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
9540	1233	RNA POLYMERASE SIGMA-70 FACTOR [PUTATIVE]	Polymerase
9546	1234	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
9554	1235	PEROXIDASE ATP2A [PUTATIVE]	Oxidase
9555	1236	VETISPIRADIENE SYNTHASE [PUTATIVE]	Synthase
9591	1237	GLUTAMATE/ORNITHINE ACETYLTRANSFERASE [PUTATIVE]	Transferases
9611	1238	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE [PUTATIVE]	Carboxylase
9612	1239	CER1-LIKE PROTEIN MAY BE INVOLVED IN WAX BIOSYNTHESIS; CONTAINS A SUR2-TYPE HYDROXYLASE/DESATURASE CATALYTIC DOMAIN (PS50242)	Desaturases
9613	1240	RECEPTOR-LIKE PROTEIN KINASE SAME AS GB:X95909 (POLYMORPHISM EXISTS AT A GA REPEAT. WE FOUND 6 COPIES IN OUR SEQUENCE WHEREAS ONLY 5 COPIES EXIST IN GB:X95909)[PUTATIVE]	Kinase, Protein

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9645	1241	ALPHA-CARBOXYLTRANSFERASE [PUTATIVE]	Transferases
9651	1242	PEPTIDE/AMINO ACID TRANSPORTER [PUTATIVE]	Transporter
9658	1243	HIGH AFFINITY CA2+ ANTIPORTER IDENTICAL TO GB:U57411, EXCEPT A POSSIBLE FRAMESHIFT AT BASE 58008. SEQUENCE HAS BEEN CONFIRMED WITH 5 SEQUENCING READS.	Transporter
9665	1244	ANTHOCYANIDIN SYNTHASE [PUTATIVE]	Synthase
9669	1245	AMMONIUM TRANSPORTER [PUTATIVE]	Transporter
9678	1246	PEROXIDASE IDENTICAL TO M58381	Oxidase
9679	1247	PEROXIDASE	Oxidase
9700	1248	ACID PHOSPHATASE CONTAINS METALLO-PHOSPHOESTERASE MOTIF (PS50185)[PUTATIVE]	Esterase
9734	1249	PHOSPHATE TRANSPORTER (ATPT2) IDENTICAL TO GB:U62331	Transporter
9743	1250	PEROXIDASE [PUTATIVE]	Oxidase
9750	1251	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9757	1252	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9758	1253	ABC TRANSPORTER [PUTATIVE]	Transporter
9766	1254	ADENYLYLATE KINASE [PUTATIVE]	Kinase
9768	1255	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE [PUTATIVE]	Transferases
9775	1256	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9779	1257	PHOSPHOLIPASE [PUTATIVE]	Lipase
9780	1258	PHOSPHOLIPASE [PUTATIVE]	Lipase
9781	1259	PHOSPHOLIPASE [PUTATIVE]	Lipase
9801	1260	BETA-1,3-ENDOGLUCANASE [PUTATIVE]	Glycosylase
9803	1261	PROTEIN KINASE [PUTATIVE]	Kinase, Protein
9815	1262	RIBONUCLEASE, RNS2 IDENTICAL TO SP:P42814:RNS2_ARATH; CONTAINS A RIBONUCLEASE T2 FAMILY HISTIDINE ACTIVE SITE SIGNATURE (PDOC00459)[PUTATIVE]	Nuclease
9822	1263	SERINE PROTEASE [PUTATIVE]	Protease

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9825	1264	PROLINE TRANSPORTER 1	Transporter
9829	1265	ISOAMYLASE [PUTATIVE]	Glycosylase
9834	1266	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE [PUTATIVE]	Transferases
9859	1267	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE [PUTATIVE]	N-Transferases
9861	1268	LIPASE/HYDROLASE GDSL-motif SIMILAR TO APG PROTEINS; PFAM DOMAIN PF00657[PUTATIVE]	Lipase
9863	1269	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9867	1270	POLYGALACTURONASE [PUTATIVE]	Glycosylase
9890	1271	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9894	1272	POTASSIUM TRANSPORTER [PUTATIVE]	Transporter
9896	1273	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9897	1274	INITIATOR tRNA PHOSPHORIBOSYL-TRANSFERASE [PUTATIVE]	Transferases
9898	1275	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9908	1276	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
9909	1277	GLYCEROL-3-PHOSPHATE DEHYDROGENASE	Dehydrogenases
9927	1278	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
9963	1279	GLUTAMATE SYNTHASE FERRODOXIN-DEPENDENT 3' PARTIAL [PUTATIVE]	Synthase
9973	1280	DNA-DIRECTED RNA POLYMERASE 23KD SUBUNIT [PUTATIVE]	Polymerase
9987	1281	PEROXIDASE [PUTATIVE]	Oxidase
9990	1282	CYTOKININ OXIDASE [PUTATIVE]	Oxidase
9993	1283	GLYCEROL-3-PHOSPHATE DEHYDROGENASE	Dehydrogenases

10007	1284	THIOREDOXIN REDUCTASE THE LAST 2 EXONS ENCODE THIOREDOXIN. THERE IS AN EST MATCH TO EXONS 5-7, AND THE DISTANCE BETWEEN EXON 7 AND EXON 8 IS ONLY 90BP. IT IS UNLIKELY THIS IS TWO SEPARATE GENES, BUT MORE LIKELY A HYBRID PROTEIN.[PUTATIVE]	Reductase
10021	1285	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10024	1286	POLYGALACTURONASE [PUTATIVE]	Glycosylase
10028	1287	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10030	1288	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10031	1289	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10032	1290	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10040	1291	PHOSPHOLIPASE D	Lipase
10066	1292	PROTEIN KINASE, 5' PARTIAL [PUTATIVE]	Kinase, Protein
10085	1293	COPPER AMINE OXIDASE [PUTATIVE]	Oxidase
10096	1294	PHOSPHOENOLPYRUVATE CARBOXYLASE	Carboxylase
10105	1295	LIPASE [PUTATIVE]	Lipase
10115	1296	CITRATE SYNTHASE [PUTATIVE]	Synthase
10127	1297	RIBOSE PHOSPHATE PYROPHOSPHOKINASE [PUTATIVE]	Kinase
10133	1298	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10141	1299	PECTINESTERASE [PUTATIVE]	Esterase
10145	1300	ISOPROPYLMALATE DEHYDRATASE [PUTATIVE]	Dehydratase
10146	1301	ISOPROPYLMALATE DEHYDRATASE	Dehydratase
10151	1302	3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT	Dehydratase
10152	1303	3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT	Dehydratase
10160	1304	CARBOXYPHOSPHONOENOLPYRUVATE MUTASE [PUTATIVE]	Mutase

10165	1305	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10177	1306	BIOTIN SYNTHASE (BIO B)	Synthase
10189	1307	PEROXIDASE [PUTATIVE]	Oxidase
10197	1308	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP TYPE [PUTATIVE]	Isomerase
10198	1309	ENDOCHITINASE [PUTATIVE]	Chitinase
10199	1310	ENDOCHITINASE [PUTATIVE]	Chitinase
10200	1311	ENDOCHITINASE [PUTATIVE]	Chitinase
10201	1312	ENDOCHITINASE [PUTATIVE]	Chitinase
10202	1313	ENDOCHITINASE [PUTATIVE]	Chitinase
10203	1314	ENDOCHITINASE [PUTATIVE]	Chitinase
10207	1315	BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT C TERMINAL HOMOLOGY ONLY[PUTATIVE]	Glycosylase
10208	1316	BETA-1,3-GLUCANASE, C TERMINAL FRAGMENT C TERMINAL HOMOLOGY ONLY[PUTATIVE]	Glycosylase
10210	1317	RECEPTOR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10211	1318	RECEPTOR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10212	1319	STEAROYL-ACP DESATURASE	Desaturases
10223	1320	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
10224	1321	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10225	1322	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
10226	1323	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10227	1324	POLYGALACTURONASE [PUTATIVE]	Glycosylase
10228	1325	POLYGALACTURONASE [PUTATIVE]	Glycosylase
10229	1326	POLYGALACTURONASE ISOLOG, 3' PARTIAL	Glycosylase
10230	1327	POLYGALACTURONASE [PUTATIVE]	Glycosylase
10232	1328	METHYL CHLORIDE TRANSFERASE [PUTATIVE]	Transferases
10234	1329	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10246	1330	6,7-DIMETHYL-8-RIBITYLLUMAZINE PRECURSOR	SYNTHASE
			Synthase

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10293	1331	HEME A: FARNESYLTRANSFERASE [PUTATIVE]	Transferases
10320	1332	FLAVONOL SYNTHASE [PUTATIVE]	Synthase
10321	1333	TRIACYLGLYCEROL LIPASE [PUTATIVE]	Lipase
10353	1334	PHOSPHATIDATE CYTIDYLTRANSFERASE [PUTATIVE]	Transferases
10360	1335	PECTINESTERASE [PUTATIVE]	Esterase
10368	1336	5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE (EPSP) SYNTHASE IDENTICAL TO GB:X06613:ATEPSPS	Synthase
10369	1337	NUCLEOTIDE SUGAR EPIMERASE [PUTATIVE]	Epimerase
10372	1338	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10377	1339	FLAVONOL REDUCTASE [PUTATIVE]	Reductase
10381	1340	DIHYDRODIPICOLINATE SYNTHASE [PUTATIVE]	Synthase
10396	1341	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10425	1342	BETA-AMYLASE [PUTATIVE]	Glycosylase
10448	1343	3-METHYL-2-OXOBUTANOATE HYDROXY-METHYL-TRANSFERASE	Transferases
10479	1344	CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
10480	1345	CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
10481	1346	CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL PROTEIN [PUTATIVE]	Channel
10508	1347	BETA-KETOACYL-COA SYNTHASE [PUTATIVE]	Synthase
10521	1348	SER/THR PROTEIN KINASE [PUTATIVE]	Kinase, Protein
10522	1349	INORGANIC PYROPHOSPHATASE 3' PARTIAL[PUTATIVE]	Phosphatase
10529	1350	PECTINESTERASE [PUTATIVE]	Esterase
10539	1351	PECTINESTERASE [PUTATIVE]	Esterase
10540	1352	PECTINESTERASE [PUTATIVE]	Esterase
10541	1353	PECTINESTERASE [PUTATIVE]	Esterase
10547	1354	ALCOHOL DEHYDROGENASE [PUTATIVE]	Dehydrogenases
10548	1355	ALCOHOL DEHYDROGENASE [PUTATIVE]	Dehydrogenases

10549	1356	ALCOHOL DEHYDROGENASE [PUTATIVE]	Dehydrogenases
10550	1357	ALCOHOL DEHYDROGENASE [PUTATIVE]	Dehydrogenases
10553	1358	GALACTINOL SYNTHASE [PUTATIVE]	Synthase
10563	1359	PECTINESTERASE [PUTATIVE]	Esterase
10567	1360	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [PUTATIVE]	Isomerase
10578	1361	HISTIDINE KINASE IDENTICAL TO GB:D87545[PUTATIVE]	Kinase, Protein
10590	1362	PECTINESTERASE [PUTATIVE]	Esterase
10594	1363	PHOTOLYASE/BLUE-LIGHT RECEPTOR (PHR2)	Receptor
10598	1364	PHOSPHOLIPASE [PUTATIVE]	Lipase
10602	1365	PECTINESTERASE [PUTATIVE]	Esterase
10608	1366	GLUTATHIONE S-TRANSFERASE (GST6) IDENTICAL TO GB:X95295. BASED ON IDENTICAL CDNA HITS, THE TRANSLATION IS NOW 40 AAS LONGER AT THE N-TERMINAL, AND START OF EXON2 IS ALSO CORRECTED.	Transferases
10628	1367	SERINE PROTEASE [PUTATIVE]	Protease
10636	1368	PROTEIN KINASE CONTAINS A PROTEIN KINASE DOMAIN PROFILE (PDOC00100)[PUTATIVE]	Kinase, Protein
10644	1369	PROTEIN KINASE	Kinase, Protein
10645	1370	EXONUCLEASE CONTAINS ZINC-FINGER C2H2-TYPE DOMAIN; SIMILAR TO X.LAEVIS XPMC2 PROTEIN (XPMC2 PREVENTS MITOTIC CATASTROPHE IN FISSION YEAST)[PUTATIVE]	Nuclease
10670	1371	GLYCOGEN SYNTHASE SIMILAR TO GLYCOGEN SYNTHASE PRECURSOR (GRANULE-BOUND STARCH SYNTHASE II) GB:Q43093 FROM [PISUM SATIVUM][PUTATIVE]	Synthase
10671	1372	PEROXIDASE VERY SIMILAR TO PEROXIDASE GB:CAA66963 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Oxidase
10678	1373	ALDOSE I-EPIMERASE SHOWS SIMILARITY TO ALDOSE EPIMERASES[PUTATIVE]	Epimerase

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10679	1374	PECTATE LYASE SIMILAR TO PECTATE LYASE PRECURSOR GB:P40973 [LILIUM LONGIFLORUM][PUTATIVE]	Lyase
10680	1375	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PORIN SIMILAR TO OUTER MITOCHONDRIAL MEMBRANE PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) GB:P42055 [SOLANUM TUBEROSUM][PUTATIVE]	Channel
10682	1376	PROTEIN KINASE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase, Protein
10691	1377	VACUOLAR MEMBRANE ATPASE SUBUNIT G (AVMA10) IDENTICAL TO VACUOLAR MEMBRANE ATPASE SUBUNIT G (AVMA10) GB:AF181688 [ARABIDOPSIS THALIANA]	GATPase
10702	1378	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR IDENTICAL TO CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR GB:P27140 [ARABIDOPSIS THALIANA]	Anhydrase
10714	1379	BETA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE GB:AAD31053 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	Transferases
10728	1380	AMINO ACID PERMEASE SIMILAR TO AMINO ACID PERMEASE GB:AAB71468 [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
10734	1381	ADENYLATE KINASE SIMILAR TO ADK. ADENYLATE KINASE GB:S50007 [STREPTOMYCES COELICOLOR][PUTATIVE]	Kinase
10736	1382	PROTEIN KINASE C-TERMINAL REGION SIMILAR TO PROTEIN KINASES: GB:S71277 [ARABIDOPSIS THALIANA], GB:CAB43834 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
10750	1383	DEHYDROGENASE CONTAINS PFAM PROFILES: PF00106 SHORT CHAIN DEHYDROGENASE, PF00678 SHORT CHAIN DEHYDROGENASE/REDUCTASE C- TERMINUS[PUTATIVE]	Dehydrogenases

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10751	1384	URIDYLIC TRANSFERASE-LIKE PROTEINS GB:AAD20075, GB: AAC00631 [ARABIDOPSIS THALIANA]; UNKNOWN PROTEIN SIMILAR TO	Transferases
10754	1385	ASPARTATE KINASE SIMILAR TO ASPARTATE KINASE GB:CAA67376 [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase
10757	1386	POTASSIUM TRANSPORTER SIMILAR TO POTASSIUM TRANSPORTER GB:AAB87687 [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
10762	1387	UDP-GLUCOSYL TRANSFERASE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GB:BAA34687, INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE GB:Q41819 [ZEA MAYS]; CONTAINS PFAM PROFILE: UDP-GLUCORONOSYL AND UDP-GLUCOSYL TRANSFERASES[PUTATIVE]	Transferases
10765	1388	PROTEIN KINASE CONTAINS PFAM PROFILE: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
10772	1389	PHYTOCHELATIN SYNTHETASE GB:CAA07251 [ARABIDOPSIS THALIANA], PFAM HMM HIT: TNFR/NGFR CYSTEINE-RICH REGION, UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Synthase
10792	1390	COESTERASE DOMAIN	Esterase
10812	1391	STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE]	Desaturases
10813	1392	STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE]	Desaturases
10814	1393	STEAROYL-ACYL CARRIER PROTEIN DESATURASE SIMILAR TO STEAROYL-ACYL CARRIER PROTEIN DESATURASE GB:CAA07349 FROM [LINUM USITATISSIMUM][PUTATIVE]	Desaturases
10825	1394	ASPARTYL PROTEASE CONTAINS PFAM PROFILE: PF00026 EUKARYOTIC ASPARTYL PROTEASE[PUTATIVE]	Protease

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10826	1395	PROTEIN PHOSPHATASE-2C (PP2C) SIMILAR TO PUTATIVE PROTEIN PHOSPHATASE-2C (PP2C) GB:AAC36699 [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE]	Phosphatase
10828	1396	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE SIMILAR TO S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE GB:P32165 [ESCHERICHIA COLI][PUTATIVE]	Transferases
10832	1397	PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
10839	1398	IAA-AMINO ACID HYDROLASE (ILR1) IDENTICAL TO IAA-AMINO ACID HYDROLASE (ILR1) GB:U23794 [ARABIDOPSIS THALIANA]	Hydrolase
10840	1399	PROTEIN KINASE CONTAINS PFAM PROFILES: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT (5 COPIES)[PUTATIVE]	Kinase, Protein
10850	1400	N-ACETLYTRANSFERASE CONTAINS PFAM PROFILE: PF00583 ACETYLTRANSFERASE (GNAT) FAMILY[PUTATIVE]	Transferases
10857	1401	CELLULOSE SYNTHASE CATALYTIC SUBUNIT SIMILAR TO CELLULOSE SYNTHASE CATALYTIC SUBUNIT GB:AAD40885 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Synthase
10871	1402	GLUTATHIONE S-TRANSFERASE IDENTICAL TO GLUTATHIONE S-TRANSFERASE GB:AAB09584 FROM [ARABIDOPSIS THALIANA]	Transferases
10906	1403	PHOSPHOLIPASE SIMILAR TO UNKNOWN PROTEIN GB:AAC32238 [ARABIDOPSIS THALIANA], POTENTIAL PHOSPHOLIPASE C- SIMILAR TO MULTIPLE PHOSPHOLIPASE PROTEINS FROM MYCOBACTERIUM SPECIES: GB:CAB06146, GB:CAB06147, GB:AAC18944, GB:CAB44656[PUTATIVE]	Lipase
10919	1404	PEROXIDASE SIMILAR TO PEROXIDASE GB:CAA66966 [ARABIDOPSIS THALIANA][PUTATIVE]	Oxidase

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10920	1405	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE SIMILAR TO PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:CAA16616 [ARABIDOPSIS THALIANA], PHOSPHORIBOSYLANTHRANILATE TRANSFERASE GB:BAA13032 [PISUM SATIVUM][PUTATIVE]	Transferases
10929	1406	SER/THR PROTEIN KINASE DOMAIN, SIMILAR TO SERINE/THREONINE PROTEIN KINASE PTO GB:AAB47421 [LYCOPERSICON ESCULENTUM]	Kinase, Protein
10930	1407	METHIONINE SYNTHASE SIMILAR TO COBALAMIN-INDEPENDENT METHIONINE SYNTHASE GB: AAC50037 [ARABIDOPSIS THALIANA][PUTATIVE]	Synthase
10950	1408	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE SIMILAR TO SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE GB:Q08632 [PICEA ABIES][PUTATIVE]	Dehydrogenase
10952	1409	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE SIMILAR TO SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE GB:Q08632 [PICEA ABIES][PUTATIVE]	Dehydrogenase
10953	1410	BETA-1,3-GLUCANASE SIMILAR TO BETA-1,3-GLUCANASE GB:S12402 [NICOTIANA SP], GB:CAA03908 [CITRUS SINENSIS], GB:S44364 [LYCOPERSICON ESCULENTUM][PUTATIVE]	Glycosylase
10963	1411	GLUTAMATE RECEPTOR (GLR1) IDENTICAL TO PUTATIVE GLUTAMATE RECEPTOR (GLR1) GB:AF079998 [ARABIDOPSIS THALIANA][PUTATIVE]	Receptor
10981	1412	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE LIPASE/ACYLHYDROLASE CONTAINS PFAM PROFILE: PF00657	Lipase
11010	1413	ETHYLENE RECEPTOR (EIN4) SIMILAR TO ETHYLENE RECEPTOR GB: AAC31123 [MALUS DOMESTICA], IDENTICAL TO PUTATIVE ETHYLENE RECEPTOR GB: AAD02485 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: RESPONSE REGULATOR RECEIVER DOMAIN, SIGNAL C TERMINAL DOMAIN[PUTATIVE]	Receptor

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11022	1414	PROTEIN KINASE SIMILAR TO HYPOTHETICAL PROTEIN WHICH CONTAINS EUKARYOTIC PROTEIN KINASE DOMAIN PF 00069 GB:CAB51834 [ORYZA SATIVA]; PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
11032	1415	RIBOSE 5-PHOSPHATE ISOMERASE IDENTICAL TO PUTATIVE RIBOSE 5-PHOSPHATE ISOMERASE GB:AAD57010 [ARABIDOPSIS THALIANA]; SIMILAR TO RIBOSE 5-PHOSPHATE ISOMERASES: GB:BAA10413 [SYNECHOCYSTIS SP], GB:CAB49687 [PYROCOCCUS ABYSSI], GB:S22097 [ESCHERICHIA COLI][PUTATIVE]	Isomerase
11040	1416	ZETA-CAROTENE DESATURASE PRECURSOR NEARLY IDENTICAL TO ZETA-CAROTENE DESATURASE PRECURSOR GB:AAA91161 [ARABIDOPSIS THALIANA][PUTATIVE]	Desaturases
11067	1417	SERINE/THREONINE PROTEIN KINASE SIMILAR TO MANY OTHER PUTATIVE PROTEIN KINASES[PUTATIVE]	Kinase, Protein
11072	1418	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE [PUTATIVE]	Transferases
11076	1419	SIGNAL PEPTIDASE MICROSOMAL GB:P28687 FROM [GALLUS GALLUS]	Protease
11079	1420	GLUCOSE AND RIBITOL DEHYDROGENASE HOMOLOG SIMILAR TO GB: AAC60580 FROM [HORDEUM VULGARE] SHOWING HOMOLOGIES TO BACTERIAL GLUCOSE AND RIBITOL DEHYDROGENASES[PUTATIVE]	Dehydrogenases
11114	1421	PECTINESTERASE SIMILAR TO PECTINESTERASE PRECURSOR GB:Q42920 FROM [MEDICAGO SATIVA][PUTATIVE]	Esterase
11115	1422	PECTINESTERASE SIMILAR TO PECTINESTERASE PPE8B PRECURSOR GB:Q43062 FROM [PRUNUS PERSICA][PUTATIVE]	Esterase
11117	1423	PROTEIN PHOSPHATASE-2C SIMILAR TO PROTEIN PHOSPHATASE-2C GB: AAC36699 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE]	Phosphatase

11144	1424	PECTINACETYLESTERASE SIMILAR TO GB:CAA67728 FROM [VIGNA RADIATA][PUTATIVE]	Esterase
11152	1425	RECEPTOR PROTEIN KINASES: GB:CAB43834, GB:S71277 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Kinase, Protein
11158	1426	ALKYL HYDROPEROXIDE REDUCTASE AND THIOL SPECIFIC ANTIOXIDANT FAMILY	Reductase
11164	1427	DUAL-SPECIFICITY PROTEIN PHOSPHATASE SIMILAR TO DUAL-SPECIFICITY PROTEIN PHOSPHATASE GB:CAA77232 [ARABIDOPSIS THALIANA][PUTATIVE]	Phosphatase
11173	1428	GUANYLATE KINASE SIMILAR TO GUANYLATE KINASE (GMK) GB:AAD31506 [SALMONELLA TYPHIMURIUM]; CONTAINS PFAM PROFILE: PF00625 GUANYLATE KINASE[PUTATIVE]	Kinase
11179	1429	GLYCOSYL TRANSFERASE CONTAINS PFAM PROFILE: PF01501 GLYCOSYL TRANSFERASE FAMILY 8[PUTATIVE]	Transferases
11180	1430	PROTEIN PHOSPHATASE-2C (PP2C) SIMILAR TO PROTEIN PHOSPHATASE-2C (PP2C) GB: AAC36699 [MESEMBRYANTHEMUM CRYSTALLINUM]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C[PUTATIVE]	Phosphatase
11183	1431	PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:P54001 [RATTUS NORVEGICUS] [UNKNOWN PROTEIN SIMILAR TO C-TERMINAL PORTION OF].	Hydroxylase
11188	1432	DEHYDROQUINASE SHIKIMATE DEHYDROGENASE SIMILAR TO DEHYDROQUINASE SHIKIMATE DEHYDROGENASE GB:S46210 [NICOTIANA TABACUM][PUTATIVE]	Dehydrogenases
11203	1433	PYRUVATE DEHYDROGENASE KINASE, 3' PARTIAL SIMILAR TO PYRUVATE DEHYDROGENASE KINASE GB: AAC97601 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Dehydrogenase
11206	1434	BETA-GLUCOSIDASE, PUTATIVE SIMILAR TO BETA-GLUCOSIDASE GB:AAF23823 FROM [ARABIDOPSIS THALIANA]	Glycosylase

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11236	1435	POLYGALACTURONASE, UNKNOWN PROTEIN CONTAINS PFAM PROFILE:PF00295	Glycosylase
11242	1436	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GB:BAA89480 FROM [SALIX GILGIANA]	Esterase
11251	1437	ASPARTATE PHOSPHATASE, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00987 RAPA-LIKE BACTERIAL PROTEIN ASPARTATE PHOSPHATASE	Phosphatase
11254	1438	TRNA PSEUDOURIDINE SYNTHASE SIMILAR TO TRNA PSEUDOURIDINE SYNTHASE A GB:P07649 [ESCHERICHIA COLI][PUTATIVE]	Synthase
11260	1439	PECTATE LYASE SIMILAR TO PECTATE LYASE 2 GB:AAF19196 [MUSA ACUMINATA][PUTATIVE]	Lyase
11261	1440	UDP-GLUCOSE:STEROL GLUCOSYLTRANSFERASE UDP-GLUCOSE:STEROL GLUCOSYLTRANSFERASE GB:Z83833 [ARABIDOPSIS THALIANA]	Transferases
11266	1441	PROTEIN KINASE SIMILAR TO APK1A PROTEIN KINASE GB:Q06548 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
11272	1442	PURPLE ACID PHOSPHATASE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 [IPOMOEA BATATAS][PUTATIVE]	Phosphatase
11275	1443	GLUCAN SYNTHASE SIMILAR TO GLUCAN SYNTHASE GB:AAD11794 [FILOBASIDIELLA NEOFORMANS VAR. NEOFORMANS][PUTATIVE]	Synthase
11286	1444	GTP CYCLOHYDROLASE I SIMILAR TO GTP CYCLOHYDROLASE I GB:P22288 [RATTUS NORVEGICUS]; CONTAINS PFAM PROFILE: PF01227 GTP CYCLOHYDROLASE I	Hydrolase
11291	1445	BETA-1,3-GLUCANASE PRECURSOR SIMILAR TO BETA-1,3-GLUCANASE PRECURSOR GB:AAD10386 [ORYZA SATIVA]; CONTAINS PFAM PROFILE: PF00332 GLYCOSYL HYDROLASES FAMILY 17[PUTATIVE]	Hydrolase
11292	1446	GLUCOSYLTRANSFERASE GB:AAD23884 [ARABIDOPSIS THALIANA], UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Transferases

11311	1447	GLUTAMATE RECEPTOR GB:AAD09173 [ARABIDOPSIS THALIANA] AND PUTATIVE LIGAND-GATED IONIC CHANNEL GB: AAC33237 [ARABIDOPSIS THALIANA], PUTATIVE	Channel
11323	1448	PREPHENATE DEHYDRATASE, P-PROTEIN: CHORISMATE MUTASE, SIMILAR TO P-PROTEIN: CHORISMATE MUTASE, PREPHENATE DEHYDRATASE GB:P43900 [HAEMOPHILUS INFLUENZAE][PUTATIVE]	Dehydratase
11327	1449	RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N-METHYLTRANSFERASE I SIMILAR TO RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N-METHYLTRANSFERASE I GB: AAC29137 [CHLOROPLAST SPINACIA OLERACEA][PUTATIVE]	Transferases
11342	1450	POLYGALACTURONASE (PGA3) IDENTICAL TO POLYGALACTURONASE (PGA3) GB: AJ005584 (MOL. GEN. GENET. 261 (6), 948-952 (1999))	Glycosylase
11343	1451	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB: CAA05892 [ARABIDOPSIS THALIANA][PUTATIVE]	Glycosylase
11344	1452	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB: CAA05892 [ARABIDOPSIS THALIANA][PUTATIVE]	Glycosylase
11345	1453	EXOPOLYGALACTURONASE IDENTICAL TO EXOPOLYGALACTURONASE GB: X72292 (MOL. GEN. GENET. 261 (6), 948-952 (1999))	Glycosylase
11357	1454	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB: AAC26512 [CUCUMIS MELO]; CONTAINS NON-CONSENSUS AA DONOR SPLIC SITE AT EXON 2[PUTATIVE]	Glycosylase
11383	1455	PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN, PF00560 LEUCINE RICH REPEAT (5 COPIES)[PUTATIVE]	Kinase, Protein
11391	1456	PROTEIN KINASE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN (2 COPIES)[PUTATIVE]	Kinase, Protein

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11398	1457	D-ALANINE:D-LACTATE LIGASE [ENTEROCOCCUS FAECIUM][HYPOTHETICAL PROTEIN SIMILAR TO]	GB:AAD41882	Ligase
11402	1458	SERINE/THREONINE PROTEIN KINASE SIMILAR TO SERINE/THREONINE-SPECIFIC KINASE GB:S68589 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: PUTATIVE SERINE/THREONINE PROTEIN KINASE, EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]		Kinase, Protein
11405	1459	BETA-GLUCAN SYNTHASE - REVERSIBLY GLYCOSYLATABLE POLYPEPTIDE SIMILAR TO REVERSIBLY GLYCOSYLATABLE POLYPEPTIDE GB:AAB88408 [PISUM SATIVUM] (POSSIBLE COMPONENT OF GOLGI [PUTATIVE])		Synthase
11413	1460	MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 SIMILAR TO MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 GB:P46972 [SACCHAROMYCES CEREVISIAE], IDENTICAL TO PUTATIVE SIGNAL PEPTIDASE GB:AAD56314 [ARABIDOPSIS THALIANA]; PFAM HMM HIT: SIGNAL PEPTIDASES I[PUTATIVE]		Protease
11416	1461	PROTEIN KINASE PFAM HMM HIT: EUKARYOTIC PROTEIN KINASE DOMAIN; SIMILAR TO PUTATIVE RECEPTOR SER/THR PROTEIN KINASE GB:AAD56317 [ARABIDOPSIS THALIANA][PUTATIVE]		Kinase, Protein
11438	1462	PROTEIN KINASE SIMILAR TO HYPOTHETICAL PROTEINS GB: AAC13615, GB:CAA18746, GB:AAB81672 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]		Kinase, Protein
11441	1463	GLUTATHIONE TRANSFERASE SIMILAR TO GLUTATHIONE TRANSFERASE GB:CAA71784 [GLYCINE MAX][PUTATIVE]		Transferases
11455	1464	PECTINACETYLESTERASE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GB:CAA67728 [VIGNA RADIATA][PUTATIVE]		Esterase
11456	1465	PECTINACETYLESTERASE SIMILAR TO PECTINACETYLESTERASE PRECURSOR GB:CAA67728 [VIGNA RADIATA][PUTATIVE]		Esterase

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11465	1466	NON-LTR REVERSE TRANSCRIPTASE SIMILAR TO PUTATIVE NON-LTR REVERSE TRANSCRIPTASE INCLUDING GB:AAD20714 AND GB:AAD24831[PUTATIVE]	Transcriptase
11472	1467	PHYTOENE DESATURASE GB:P28553 FROM [GLYCINE MAX][PUTATIVE, OXIDOREDUCTASE SIMILAR TO]	Desaturases
11478	1468	ASCORBATE PEROXIDASE STRONG SIMILARITY TO ASCORBATE PEROXIDASE GB:CAA56340[PUTATIVE]	Oxidase
11497	1469	PROTEIN KINASE SIMILAR TO PROTEIN KINASE (APK1A) GB:Q06548 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN[PUTATIVE]	Kinase, Protein
11507	1470	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
11515	1471	ENDONUCLEASE III HOMOLOGS: GB:AAD35453, GB:BAA79061, GB:CAB49586[HYPOTHETICAL PROTEIN SIMILAR TO]	Nuclease
11517	1472	URIDYLATE KINASE SIMILAR TO URIDYLATE KINASE GB:CAB13524 [BACILLUS SUBTILIS], GB:P74457 [SYNECHOCYSTIS PCC6803][PUTATIVE]	Kinase
11520	1473	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, UNKNOWN PROTEIN PFAM HMM HIT:	Isomerase
11537	1474	LYCOPENE BETA CYCLASE IDENTICAL TO LYCOPENE BETA CYCLASE GB:AAB53337 [ARABIDOPSIS THALIANA]	Cyclase
11542	1475	FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE I SIMILAR TO FATTY ACID ELONGASE 3-KETOACYL-COA SYNTHASE I GB:AAC99312 [ARABIDOPSIS THALIANA][PUTATIVE]	Synthase
11576	1476	DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE SIMILAR TO DIADENOSINE 5',5"-P1,P4-TETRAPHOSPHATE HYDROLASE GB:AAC49902 [LUPINUS ANGUSTIFOLIUS], PFAM HMM HIT: BACTERIAL MUTT PROTEIN[PUTATIVE]	Hydrolase

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11577	1477	MANNOSYLTRANSFERASE [ESCHERICHIA COLI], UNKNOWN PROTEIN C- TERMINAL PORTION SIMILAR TO	GB:BAA28328	Transferases
11581	1478	ABC TRANSPORTER ATPASE SIMILAR TO ABC TRANSPORTER ATPASE GB: AAC68280 [CHLAMYDIA TRACHOMATIS][PUTATIVE]		Transporter
11584	1479	GALACTOKINASE, 5' PARTIAL SIMILAR TO GALACTOKINASE GB:BAA84705 [MUS MUSCULUS][PUTATIVE]		Kinase
11585	1480	PECTINESTERASE CONTAINS SIMILARITY TO PECTINESTERASE GB:AAB57671 [CITRUS SINENSIS][PUTATIVE]		Esterase
11586	1481	PECTINESTERASE CONTAINS SIMILARITY TO PECTINESTERASE GB:AAB57671 [CITRUS SINENSIS][PUTATIVE]		Esterase
11588	1482	ALPHA-L-ARABINOFRANOSIDASE CONTAINS SIMILARITY TO ALPHA-L-ARABINOFRANOSIDASE A PRECURSOR GB:P42254 [ASPERGILLUS NIGER][PUTATIVE]		Glycosylase
11598	1483	ALPHA/BETA HYDROLASE CONTAINS PFAM PROFILE: PF00561 ALPHA/BETA HYDROLASE FOLD; PREDICTED BY GENSCAN[PUTATIVE]		Hydrolase
11601	1484	ALPHA-HYDROXYNITRILE LYASE SIMILAR TO ALPHA- HYDROXYNITRILE LYASE GB:CAA11219 [MANIHOT ESCULENTA][PUTATIVE]		Lyase
11603	1485	(1-4)-BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 [LYCOPERSICON ESCULENTUM][PUTATIVE]		Hydrolase
11604	1486	(1-4)-BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 [LYCOPERSICON ESCULENTUM][PUTATIVE]		Hydrolase
11631	1487	LEUCANTHOCYANIDIN DIOXYGENASE, PUTATIVE SIMILAR TO LEUCANTHOCYANIDIN DIOXYGENASE SP:P51093 [VITIS VINIFERA (GRAPE)]		Oxygenases

11645	1488	GLUCOSYL TRANSFERASE, PUTATIVE SIMILAR TO ZEATIN O-XYLOSYLTRANSFERASE SP:P56725 [PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)]	Transferases
11651	1489	PROTEIN PHOSPHATASE 2C (PP2C) IDENTICAL TO PROTEIN PHOSPHATASE 2C (PP2C) GB:P49598 [ARABIDOPSIS THALIANA]	Phosphatase
11676	1490	DIGALACTOSYLDIACYLGLYCEROL SYNTHASE IDENTICAL TO DIGALACTOSYLDIACYLGLYCEROL SYNTHASE GB:AAD42378 [ARABIDOPSIS THALIANA]	Synthase
11684	1491	DIHYDRONEOPTERIN ALDOLASE SIMILAR TO DIHYDRONEOPTERIN ALDOLASE GB:P28823 [BACILLUS SUBTILIS][PUTATIVE]	Aldolase
11714	1492	DNA-3-METHYLADENINE GLYCOSYLASE (MAG) IDENTICAL TO DNA-3-METHYLADENINE GLYCOSYLASE (MAG) SP:Q39147 [ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)]	Glycosylase
11743	1493	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP- TYPE, PUTATIVE CONTAINS PFAM PROFILE:PF00254 FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	Isomerase
11759	1494	CHITINASE BASIC, IDENTICAL TO BASIC CHITINASE GB:AAA32769 GI:166666 [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 93, 907-914 (1990))	Chitinase
11771	1495	PROTEIN PHOSPHATASE 2C, PUTATIVE CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C	Phosphatase
11784	1496	ZINC TRANSPORTER IDENTICAL TO PUTATIVE ZINC TRANSPORTER GB:AAC24197 FROM [ARABIDOPSIS THALIANA], (PROC. NATL. ACAD. SCI. U.S.A. 95 (12), 7220-7224 (1998))[PUTATIVE]	Transporter
11796	1497	OXIDOREDUCTASES[HYPOTHETICAL SIMILAR TO] PROTEIN	Reductase
11799	1498	OXIDOREDUCTASES[HYPOTHETICAL SIMILAR TO] PROTEIN	Reductase
11816	1499	PROTEIN KINASE, 3' PARTIAL LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1 GB: AAC27894 FROM [ZEA MAYS][PUTATIVE]	Kinase, Protein

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11818	1500	ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER	Transporter
11819	1501	ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER	Transporter
11820	1502	ABC TRANSPORTER, PUTATIVE SIMILAR TO ATMRP4 (TRANSPORT OF GLUTATHIONE-CONJUGATES INTO THE VACUOLE) GB:CAA05625 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00005 ABC TRANSPORTER	Transporter
11821	1503	SERINE ACETYLTRANSFERASE (SAT-1) IDENTICAL TO SERINE ACETYLTRANSFERASE (SAT-1) GB:U22964 [ARABIDOPSIS THALIANA] (PLANT MOL. BIOL. 30 (5), 1041-1049 (1996))	Transferases
11843	1504	LOW AFFINITY CALCIUM ANTIPORTER CAX2 ALMOST IDENTICAL TO GB:AAB05914 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILE: PF00002 7 TRANSMEMBRANE RECEPTOR (SECRETIN FAMILY), AND PF01699 SODIUM/CALCIUM EXCHANGER PROTEIN	Transporter
11849	1505	BRASSINOSTEROID RECEPTOR KINASE, PUTATIVE SIMILAR TO GB:AAC49810 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILES: PF00560 LEUCINE RICH REPEAT (23 COPIES)	Kinase, Protein
11850	1506	L-ASCORBATE OXIDASE PRECURSOR, PUTATIVE SIMILAR TO GB:Q00624 FROM [BRASSICA NAPUS] (PLANT J. 2 (3), 331-342 (1992))	Oxidase
11851	1507	POLLEN SPECIFIC PROTEIN, PUTATIVE SIMILAR TO GB:CAB59910 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILES: PF00394 MULTICOPPER OXIDASE	Oxidase

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11868	1508	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR, PUTATIVE SIMILAR TO GB:P52409 FROM [TRITICUM AESTIVUM]	Glycosylase
11874	1509	TRANSPORTER PROTEINS[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transporter
11887	1510	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
11899	1511	BETA-FRUCTOFURANOSIDASE, PUTATIVE SIMILAR TO BETA-FRUCTOFURANOSIDASE 1 GB:S37212 FROM [ARABIDOPSIS THALIANA]	Glycosylase
11900	1512	BETA-FRUCTOFURANOSIDASE 1 IDENTICAL TO GB:S37212 FROM [ARABIDOPSIS THALIANA]	Glycosylase
11901	1513	HYDROLASE, PUTATIVE SIMILAR TO METAL DEPENDENT HYDROLASE GB:AAD18619 FROM [CHLAMYDOPHILA PNEUMONIAE]	Hydrolase
11925	1514	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB:CAA11160 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Glycosylase
11926	1515	GTP PYROPHOSPHOKINASE SIMILAR TO GTP PYROPHOSPHOKINASE GB:O87331 FROM [CORYNEBACTERIUM GLUTAMICUM][PUTATIVE]	Kinase
11928	1516	PROTEASE, 5'PARTIAL SIMILAR TO SERINE PROTEASE GB:CAA07250 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE]	Protease
11944	1517	LIPASE/HYDROLASE GD\$L-LIKE MOTIF; MYROSINASE- ASSOCIATED PROTEIN, PUTATIVE SIMILAR TO GB:CAA71238 FROM [BRASSICA NAPUS], CONATAINS PFAM PROFILE:PF00657	Lipase
11954	1518	PECTIN METHYLESTERASE SIMILAR TO PECTINESTERASE GB:Q43867 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Esterase
11955	1519	PECTIN METHYLESTERASE SIMILAR TO PECTIN METHYLESTERASE GB:Q42534 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Esterase

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11959	1520	LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE SIMILAR TO LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE 1 GB: AAC27894 FROM [ZEA MAYS][PUTATIVE]	Kinase, Protein
11963	1521	DIAMINOPIMELATE DECARBOXYLASE SIMILAR TO DIAMINOPIMELATE DECARBOXYLASE GB: CAB62550 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Decarboxylase
11970	1522	9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO 9-CIS-EPOXYCAROTENOID DIOXYGENASE GB: AAF26356 [PHASEOLUS VULGARIS]	Oxygenases
11975	1523	TERPENE SYNTHASE-RELATED PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase
11977	1524	GERANYLGERANYL PYROPHOSPHATE SYNTHETASE, PUTATIVE SIMILAR TO GERANYLGERANYL PYROPHOSPHATE SYNTHETASE GB: P34802 [ARABIDOPSIS THALIANA]	Synthase
11978	1525	TERPENE SYNTHASE GB: CAA72074 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase
11979	1526	GERANYLGERANYL PYROPHOSPHATE SYNTHASE GGPS3 ALMOST IDENTICAL TO GB: S71231 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Synthase
11980	1527	TERPENE SYNTHASE GB: CAA72074 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase
11981	1528	GERANYLGERANYL PYROPHOSPHATE SYNTHASE GGPS3 ALMOST IDENTICAL TO GB: S71231 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Synthase
11983	1529	GLUCAN SYNTHASES[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Synthase
12004	1530	CALLOSE SYNTHASE CATALYTIC SUBUNIT-LIKE PROTEIN GB: CAB88264 GI: 7630056 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Synthase

12010	1531	RECEPTOR-LIKE SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO RECEPTOR-LIKE SERINE/THREONINE KINASE GB: AAC50043 GI: 2465923 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
12015	1532	DNA-LIGASE ZN-FINGER REGION (REGION ACTS AS A DNA NICK SENSOR) (3 COPIES AT N-TERMINUS)	Ligase
12020	1533	PHOSPHOENOLPYRUVATE CARBOXYLASE (PPC) IDENTICAL TO PHOSPHOENOLPYRUVATE CARBOXYLASE (PPC) GB: AF071788 [ARABIDOPSIS THALIANA]	Carboxylase
12022	1534	GALACTOSYLTRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01762 GALACTOSYLTRANSFERASE; SIMILAR TO AVR9 ELICITOR RESPONSE PROTEIN GB: CAA06925 [NICOTIANA TABACUM]	Transferases
12053	1535	PROTEIN PHOSPHATASE TYPE 2C SIMILAR TO PROTEIN PHOSPHATASE TYPE 2C GB: AAD17805 FROM [LOTUS JAPONICUS][PUTATIVE]	Phosphatase
12088	1536	PHOSPHATIDYLINOSITOL 3- AND 4-KINASE HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF00454	Kinase
12095	1537	LYSOPHOSPHOLIPASE SIMILAR TO LYSOPHOSPHOLIPASE GB: AAD52700 [SCHISTOSOMA JAPONICUM][PUTATIVE]	Lipase
12099	1538	ACETYL-COA CARBOXYLASE BIOTIN-CONTAINING SUBUNIT SIMILAR TO ACETYL-COA CARBOXYLASE BIOTIN-CONTAINING SUBUNIT GB: AAC49114 [ARABIDOPSIS THALIANA]; CONTAINS PFAM PROFILE: PF00364 BIOTIN-REQUIRING ENZYMES[PUTATIVE]	Carboxylase
12102	1539	POLYGALACTURONASE SIMILAR TO POLYGALACTURONASE GB: BAA88472 [CUCUMIS SATIVUS][PUTATIVE]	Glycosylase
12110	1540	BETA-1,3-GLUCANASE PRECURSOR SIMILAR TO BETA-1,3-GLUCANASE PRECURSOR GB: AAD10386 [ORYZA SATIVA][PUTATIVE]	Glycosylase
12119	1541	PROTEIN KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB: AAB61708 FROM [DAUCUS CAROTA]	Kinase, Protein

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12124	1542	GLYCOSYL TRANSFERASES GROUP 1, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE:PF00534	Transferases
12133	1543	RECEPTOR KINASE SIMILAR TO RECEPTOR KINASE GB:S70769 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Kinase, Protein
12166	1544	LIPASE/HYDROLASE GDSL-LIKE MOTIF; PUTATIVE CONTAINS PFAM PROFILE: PF00657 LIPASE/ACYLHYDROLASE	Lipase
12181	1545	GLUCOSYLTRANSFERASE SIMILAR TO UDP-GLUCOSE GLUCOSYLTRANSFERASE GB:X77459 [MANIHOT ESCULENTA], UDP-GLYCOSE:FLAVONOID GLYCOSYLTRANSFERASE GB:BAA36411 [VIGNA MUNGO][PUTATIVE]	Transferases
12183	1546	SERINE PROTEASE SIMILAR TO HUMAN HTRA SERINE PROTEASE GB: AAC97211 [HOMO SAPIENS][PUTATIVE]	Protease
12184	1547	SERINE PROTEASE SIMILAR TO HUMAN HTRA SERINE PROTEASE GB: AAC97211 [HOMO SAPIENS][PUTATIVE]	Protease
12186	1548	PROTEIN PHOSPHATASE 2C DOMAIN	Phosphatase
12211	1549	PROTEIN PHOSPHATASE, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GB: AAC36699 FROM [MESEMBRYANTHEMUM CRYSTALLNUM]	Phosphatase
12216	1550	POLYGALACTURONASE, PUTATIVE SIMILAR TO ENDOPOLYGALACTURONASE GB:225933 FROM [LYCOPERSICON ESCULENTUM]	Glycosylase
12224	1551	ACYL-COA SYNTHETASE, AMP-BINDING PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF00501 AMP- BINDING ENZYME; SIMILAR TO ACYL-COA SYNTHETASE GB:CAB54055 [PSEUDOMONAS PUTIDA]	Synthase
12225	1552	CHITINASE BASIC, PUTATIVE SIMILAR TO BASIC CHITINASE GB:CAA78843 [LYCOPERSICON ESCUENTUM] (PLANT MOL. BIOL. 22 (6), 1017-1029 (1993))	Chitinase
12239	1553	PECTINESTERASE, PUTATIVE SIMILAR TO PECTINESTERASE GB:AAB57669 [CITRUS SINENSIS]; CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE	Esterase

12240	1554	PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE GB:AAD37376 [GLYCINE MAX]	Oxidase
12242	1555	PROTEIN PHOSPHATASE-2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE-2C GB: AAC35951 [MESEMBRYANTHEMUM CRYSTALLINUM]; CONTAINS PFAM PROFILE: PF00481 PROTEIN PHOSPHATASE 2C	Phosphatase
12253	1556	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASES[HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase
12260	1557	PROTEIN PHOSPHATASE SIMILAR TO PROTEIN PHOSPHATASE-2C GB: AAC36698 FROM [MESEMBRYANTHEMUM CRYSTALLINUM][PUTATIVE]	Phosphatase
12266	1558	DNA METHYLASE DOMAIN	Methylase
12277	1559	SERINE/THREONINE PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
12306	1560	ION CHANNEL PROTEIN FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Channel
12307	1561	ION CHANNEL PROTEIN FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Channel
12309	1562	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) GB:P54767 [LYCOPERSICON ESCULENTUM]; SIMILAR TO N-TERMINAL PORTION OF	Decarboxylase
12313	1563	GLUTAMATE DECARBOXYLASE, PUTATIVE SIMILAR TO GLUTAMATE DECARBOXYLASE GB:Q07346 [PETUNIA X HYBRIDA] (J. BIOL. CHEM. 268 (26), 19610-19617 (1993))	Decarboxylase
12316	1564	ACID PHOSPHATASE TYPE 5 IDENTICAL TO GB:CAB63938 FROM [ARABIDOPSIS THALIANA]	Phosphatase
12333	1565	AMIDASE, PUTATIVE SIMILAR TO AMIDASE GB:AAA26183 FROM [RHODOCOCCUS SP.]	AMIDASE

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12361	1566	DIACYLGLYCEROL PYROPHOSPHATE PHOSPHATASE, PUTATIVE SIMILAR TO GB:NP_010570 FROM [SACCHAROMYCES CEREVISIAE], CONTAINS PFAM PROFILE: PF01569 PHOSPHATASE PAP2 SUPERFAMILY	Phosphatase
12366	1567	MANDELATE RACEMASE/MUCONATE LACTONIZING ENZYME FAMILY, UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF01188	Epimerase
12383	1568	PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT CALCINEURIN B SUBUNIT GB:P42322 FROM [NAEGLERIA GRUBERI] (GENE 154 (1), 39-45 (1995))	Phosphatase
12389	1569	ASPARTYL PROTEASE, CHLOROPLAST NUCLEOID DNA-BINDING PROTEIN SIMILAR TO GB:BAA22813 FROM [NICOTIANA TABACUM] (PLANT CELL 9 (9), 1673-1682 (1997)), CONTAINS PFAM PROFILE: PF00026 EUKARYOTIC ASPARTYL PROTEASE[PUTATIVE]	Protease
12410	1570	URIDYLATE KINASE, PUTATIVE SIMILAR TO UMP-KINASE GB:CAB38122 FROM [LACTOCOCCUS LACTIS]	Kinase
12423	1571	PROTEIN KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB:AAB61708 FROM [DAUCUS CAROTA]	Kinase, Protein
12442	1572	FLAVANONE-3-HYDROXYLASE GB:Q05965 FROM [MATTHIOLA INCANA], CONTAINS PFAM PROFILE: PF00671 IRON/ASCORBATE OXIDOREDUCTASE FAMILY[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Hydroxylase
12443	1573	FLAVONOL SYNTHASE (FLS) GB:Q41452 FROM [SOLANUM TUBerosum], CONTAINS PFAM PROFILE: PF00671 IRON/ASCORBATE OXIDOREDUCTASE FAMILY[HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Synthase
12445	1574	PHOSPHOSERINE AMINOTRANSFERASE GB:P19689 FROM [YERSINIA ENTEROCOLITICA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO]	Transferases
12459	1575	TRNA ISOPENTENYL TRANSFERASE, PUTATIVE SIMILAR TO TRNA ISOPENTENYL TRANSFERASE GB:AAF00582 FROM [ARABIDOPSIS THALIANA]	Transferases

12471	1576	FUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FUCT C3 PROTEIN GB:CAB52254 FROM [VIGNA RADIATA] (J. BIOL. CHEM. (1999) 274 (31), 21830-21839)	Transferases
12488	1577	CINNAMYL ALCOHOL DEHYDROGENASE IDENTICAL TO GB:P48523 FROM [ARABIDOPSIS THALIANA]	Dehydrogenases
12501	1578	AMINO ACID PERMEASE, PUTATIVE, 5' PARTIAL CONTAINS PFAM PROFILE: PF00324 AMINO ACID PERMEASE	Transporter
12508	1579	BETA-XYLOSIDASE, PUTATIVE SIMILAR TO BETA-XYLOSIDASE A GB:BAA28267 FROM [ASPERGILLUS ORYZAE]	Glycosylase
12516	1580	RECEPTOR-LIKE PROTEIN KINASE, PUTATIVE SIMILAR TO LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE GB:AAC36318 FROM [MALUS DOMESTICA]	Kinase, Protein
12564	1581	GERANYL GERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYL GERANYL PYROPHOSPHATE SYNTHASE GB:BAA23157 [ARABIDOPSIS THALIANA]	Synthase
12567	1582	RECEPTOR KINASE PROTEIN, PUTATIVE SIMILAR TO RECEPTOR KINASE GB:AAA33715 [PETUNIA INTEGRIFOLIA]	Kinase, Protein
12572	1583	MITOCHONDRIAL CARRIER PROTEIN, PUTATIVE CONTAINS PFAM PROFILE: PF00153 MITOCHONDRIAL CARRIER PROTEINS	Transporter
12597	1584	TETRAACYLDISACCHARIDE 4'-KINASE GB:P27300 [ESCHERICHIA COLI][HYPOTHETICAL PROTEIN SIMILAR TO]	Kinase
12599	1585	PURPLE ACID PHOSPHATASE, PUTATIVE SIMILAR TO PURPLE ACID PHOSPHATASE GB:CAA06921 [IPOMOEA BATATAS]	Phosphatase
12602	1586	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
12627	1587	DNA TOPOISOMERASE VI SUBUNIT B TYPE II GB:O05207 FROM [SULFOLOBUS SHIBATAE], UNKNOWN PROTEIN SIMILAR TO	Isomerase

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12662	1588	PHOSPHORIBOSYAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE, PUTATIVE SIMILAR TO PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE GB:P38025 FROM [ARABIDOPSIS THALIANA]	Synthase
12676	1589	ABC TRANSPORTER GB: AAC49791 FROM [ARABIDOPSIS THALIANA], SIMILAR TO MRP-LIKE	Transporter
12685	1590	SERINE/THREONINE-SPECIFIC PROTEIN KINASE, PUTATIVE SIMILAR TO SERINE/THREONINE-SPECIFIC PROTEIN KINASE GB:T02731 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
12693	1591	IRON/ASCORBATE OXIDOREDUCTASE FAMILY	Reductase
12696	1592	PROTEIN KINASE DOMAIN	Kinase, Protein
12698	1593	ADENYL CYCLASE, PUTATIVE, 3' PARTIAL SIMILAR TO ADENYL CYCLASE GB:AAB87670 FROM [NICOTIANA TABACUM]	Cyclase
12699	1594	ADENYL CYCLASE, PUTATIVE, 5' PARTIAL SIMILAR TO ADENYL CYCLASE GB:AAB87670 [NICOTIANA TABACUM]	Cyclase
12703	1595	1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE GB:AAD38941 [LYCOPERSICON ESCULENTUM]	Synthase
12709	1596	UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO UDP-GLUCOSE:INDOLE-3-ACETATE GLUCOSYLTRANSFERASE GB:AAB58497	BETA-D-Transfases
12717	1597	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE, PUTATIVE CONTAINS PFAM PROFILE: PF00254 FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASES	Isomerase
12728	1598	UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE]	Transfases
12729	1599	UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE]	Transfases

12730	1600	PEROXIDASE ALMOST IDENTICAL TO GB:CAA66965 AND GB:CAA67360 FROM [ARABIDOPSIS THALIANA][PUTATIVE]	Oxidase
12731	1601	UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE]	Transferases
12732	1602	UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE]	Transferases
12733	1603	UDP-GLUCOSE GLUCOSYLTRANSFERASE SIMILAR TO GB:Q40284 FROM [MANIHOT ESCULENTA][PUTATIVE]	Transferases
12749	1604	SALICYLIC ACID CARBOXYL METHYLTRANSFERASE, PUTATIVE SIMILAR TO GB:AAF00108 FROM [CLARKIA BREWERI]	Transferases
12792	1605	ALTERNATIVE OXIDASE 1B PRECURSOR IDENTICAL TO GB:O23913 FROM [ARABIDOPSIS THALIANA]	Oxidase
12793	1606	ALTERNATIVE OXIDASE 1A PRECURSOR IDENTICAL TO GB:Q39219 FROM [ARABIDOPSIS THALIANA]	Oxidase
12813	1607	ACETYLTRANSFERASE (GNAT) FAMILY; HYPOTHETICAL PROTEIN PREDICTED BY GENEMARK.HMM, CONTAINS PFAM PROFILE:PF00583 ACETYLTRANSF	Transferases
12849	1608	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (SUBUNIT 5) GB:P46279 [GLYCINE MAX][HYPOTHETICAL PROTEIN SIMILAR TO]	Polymerase
12875	1609	ETHYLENE RECEPTOR, PUTATIVE (ETR2) SIMILAR TO ETHYLENE RECEPTOR HOMOLOG GB:AAD31396 FROM [LYCOPERSICON ESCULENTUM], CONTAINS PFAM PROFILE: PF01590 GAF DOMAIN	Receptor
12897	1610	PROTEIN PHOSPHATASE GB:AADI7805 FROM [LOTUS JAPONICUS]	Phosphatase
12902	1611	GMC OXIDOREDUCTASE DOMAIN	Reductase
12910	1612	CYANATE LYASE (CYN) IDENTICAL TO CYANASE (CYN) GB:AB004568 [ARABIDOPSIS THALIANA]	Lyase
12918	1613	DIENELACTONE HYDROLASE FAMILY	Hydrolase
12921	1614	DIENELACTONE HYDROLASE FAMILY	Hydrolase

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12922	1615	DUAL-SPECIFICITY PROTEIN PHOSPHATASE IDENTICAL TO DSPTP1 PROTEIN GB:CAA77232 FROM [ARABIDOPSIS THALIANA]	Phosphatase
12924	1616	IPP TRANSFERASE, HYPOTHETICAL PROTEIN CONTAINS PFAM PROFILE: PF01715	Transferases
12926	1617	PROTEIN KINASE GB:AAD24596 FROM [ARABIDOPSIS THALIANA] [HYPOTHETICAL PROTEIN SIMILAR TO] [PUTATIVE]	Kinase, Protein
12934	1618	XYLOGLUCAN ENDOTRANSGLYCOSYLASE, PUTATIVE SIMILAR TO XYLOGLUCAN ENDOTRANSGLYCOSYLASE 1 GB:CAA10231 FROM [FAGUS SYLVATICA] (PLANT PHYSIOL.(1999) 119, 1148-1148)	Glycosylase
12936	1619	RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO TMK GB:CAA69028 FROM [ORYZA SATIVA]	Kinase, Protein
12938	1620	BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA-1,3-GLUCANASE GB:BAA89481 FROM [SALIX GILGIANA]	Glycosylase
12943	1621	NAD DEPENDENT EPIMERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01370 NAD DEPENDENT EPIMERASE/DEHYDRATASE FAMILY	Dehydratase
12953	1622	BETA-AMYLASE, PUTATIVE SIMILAR TO BETA-AMYLASE GB:CAB58423 [ARABIDOPSIS THALIANA]	Glycosylase
12955	1623	DIHYDROXYACID DEHYDRATASE, PUTATIVE SIMILAR TO DIHYDROXYACID DEHYDRATASE GB:CAA60939 [SACCHAROMYCES CEREVISIAE]	Dehydratase
12964	1624	HYDROXYETHYLTHIAZOLE KINASE, PUTATIVE SIMILAR TO HYDOXYETHYLTHIAZOLE KINASE (THIM) GB:BAA76743 [ESCHERICHIA COLI]	Kinase
12965	1625	MUCIN CORE 2 BETA 6-N-ACETYLGLUCOSAMINYLTRANSFERASE GB:AAA83244 [BOS TAURUS] [HYPOTHETICAL PROTEIN SIMILAR TO]	Transferases
12974	1626	PECTINESTERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE	Esterase

12983	1627	9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE SIMILAR TO GB:CAB10168 FROM [LYCOPERSICON ESCULENTUM] (J. EXP. BOT. 47, 2111-2112 (1997))	Oxygenases
12984	1628	PECTATE LYASE, PUTATIVE SIMILAR TO GB:AAF19196 FROM [MUSA ACUMINATA]	Lyase
12986	1629	RECEPTOR KINASE, PUTATIVE SIMILAR TO CLV1 RECEPTOR KINASE GB:AAB58929 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
12988	1630	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB: AAC63678 GI:3738337 FROM [ARABIDOPSIS THALIANA], HYPOTHETICAL PROTEIN, 3' PARTIAL SIMILAR TO PUTATIVE	Transcriptase
12996	1631	BETA-1,3-GLUCANASE, PUTATIVE SIMILAR TO BETA- 1,3-GLUCANASE GB:BAA89481 FROM [SALIX GILGIANA]	Glycosylase
13003	1632	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
13005	1633	ALPHA/BETA HYDROLASE FOLD	Hydrolase
13017	1634	PROTEIN KINASE, PUTATIVE SIMILAR TO GB:BAA24694 FROM [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL. 38 (3), 248-258 (1997))	Kinase, Protein
13018	1635	PROTEIN KINASE, PUTATIVE SIMILAR TO GB:BAA24694 FROM [ARABIDOPSIS THALIANA] (PLANT CELL PHYSIOL. 38 (3), 248-258 (1997))	Kinase, Protein
13022	1636	PROCESSING PEPTIDASE, CHLOROPLAST THYLAKOIDAL PROCESSING PEPTIDASE, PUTATIVE SIMILAR TO GB:CAA71502 FROM [ARABIDOPSIS THALIANA]	Protease
13029	1637	KINASE-LIKE PROTEIN TMKLI PRECURSOR IDENTICAL TO PUTATIVE KINASE-LIKE PROTEIN TMKLI PRECURSOR GB:P33543 FROM [ARABIDOPSIS THALIANA], (PLANT MOL. BIOL. 23 (2), 415-421 (1993))[PUTATIVE]	Kinase, Protein
13030	1638	PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GB:AAB71208 FROM [FRAGARIA ANANASSA], (PLANT MOL. BIOL. 34 (6), 867-877 (1997))	Lyase

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13034	1639	NADPH-FERRIHEMOPROTEIN GB:AAF02110 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	REDUCTASE	Reductase
13043	1640	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE GB:BAA24694 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein	
13061	1641	ENDOXYLOGLUCAN TRANSFERASE, PUTATIVE SIMILAR TO GB:C49539 FROM [ARABIDOPSIS THALIANA] (J. BIOL. CHEM. 268 (34), 25364-25368 (1993))	Transferases	
13067	1642	ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE IDENTICAL TO ACYL-(ACYL CARRIER PROTEIN) THIOESTERASE GB:Z36912 [ARABIDOPSIS THALIANA] (ARCH. BIOCHEM. BIOPHYS. 316 (1), 612-618 (1995))	Esterase	
13070	1643	GLYCOSYL TRANSFERASE, PUTATIVE CONTAINS PFAM PROFILE: PF01501 GLYCOSYL TRANSFERASE FAMILY 8	Transferases	
13084	1644	REVERSE TRANSCRIPTASE GB:S65812 [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO]	Transcriptase	
13085	1645	NITRATE TRANSPORTER, PUTATIVE SIMILAR TO NITRATE TRANSPORTER (NTL1) GB:AAC28086 [ARABIDOPSIS THALIANA]	Transporter	
13088	1646	BILE ACID SODIUM SYMPORter FAMILY	Transporter	
13096	1647	WALL-ASSOCIATED SERINE/THREONINE KINASE, PUTATIVE SIMILAR TO WALL-ASSOCIATED KINASE 4 GB:CAA08793 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein	
13103	1648	SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, PUTATIVE SIMILAR TO SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE GB:AAB61708 FROM [DAUCUS CAROTA]	Kinase, Protein	
13129	1649	TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase	
13130	1650	TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase	

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13131	1651	LIMONENE CYCLASE, PUTATIVE, 5' PARTIAL SIMILAR TO LIMONENE CYCLASE GB:BAA08367 FROM [PERILLA FRUTESCENS]	Cyclase
13132	1652	LIMONENE CYCLASE, PUTATIVE SIMILAR TO LIMONENE CYCLASE GB:BAA08367 FROM [PERILLA FRUTESCENS],..CONTAINS. PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase
13165	1653	CELLULASE, PUTATIVE CONTAINS PFAM PROFILE: PF00150 CELLULASE (GLYCOSYL HYDROLASE FAMILY 5)	Hydrolase
13166	1654	CELLULASE, PUTATIVE CONTAINS PFAM PROFILE: PF00150 CELLULASE (GLYCOSYL HYDROLASE FAMILY 5)	Hydrolase
13190	1655	ALPHA GALACTOSIDASE GB:AAA73963 [GLYCINE MAX}, UNKNOWN PROTEIN SIMILAR TO	Glycosylase
13214	1656	POLYGALACTURONASE, PUTATIVE SIMILAR TO POLYGALACTURONASE (PG1) GB:AAD46483 [GLYCINE MAX]	Glycosylase
13226	1657	PROTEIN KINASE, PUTATIVE CONTAINS PFAM PROFILE: PF00069 EUKARYOTIC PROTEIN KINASE DOMAIN	Kinase, Protein
13228	1658	ALPHA-MANNOSIDASE, PUTATIVE SIMILAR TO LYSOSOMAL ALPHA-MANNOSIDASE GB: AAC34130 [HOMO SAPIENS] (HUM. MOL. GENET. 6 (5), 717-726 (1997))	Glycosylase
13234	1659	SHORT CHAIN ALCOHOL DEHYDROGENASE CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE; SIMILAR TO SEX DETERMINATION PROTEIN TASSELSEED 2 GB:P50160 [ZEA MAYS][PUTATIVE]	Dehydrogenase
13235	1660	SHORT CHAIN ALCOHOL DEHYDROGENASE CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE; SIMILAR TO SEX DETERMINATION PROTEIN TASSELSEED 2 GB:P50160 [ZEA MAYS][PUTATIVE]	Dehydrogenase
13240	1661	ALPHA/BETA HYDROLASE FOLD	Hydrolase

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13248	1662	SHIKIMATE KINASE SIMILAR TO SHIKIMATE KINASE PRECURSOR GB:CAA45121 [LYCOPERSICON ESCULENTUM][PUTATIVE]	Kinase
13254	1663	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
13271	1664	PEPTIDASE FAMILY M48	Protease
13274	1665	PROTEIN PHOSPHATASE 2C, PUTATIVE SIMILAR TO PROTEIN PHOSPHATASE 2C GB:T09640 FROM [MEDICAGO SATIVA]	Phosphatase
13292	1666	ESTERASE, PUTATIVE SIMILAR TO ESTERASE HDE GB:BAA82510 FROM [PETROLEUM-DEGRADING BACTERIUM HD-1]	Esterase
13302	1667	PECTATE LYASE, PUTATIVE SIMILAR TO PECTATE LYASE GB:CAA70735 [ZINNIA ELEGANS] (PLANT J. 13 (1), 17-28 (1998)); CONTAINS PFAM PROFILE: PF00544 PECTATE LYASE	Lyase
13326	1668	ALTERNATIVE OXIDASE 1C PRECURSOR IDENTICAL TO ALTERNATIVE OXIDASE 1C PRECURSOR GB:O22048 FROM [ARABIDOPSIS THALIANA]	Oxidase
13355	1669	NADPH:QUINONE OXIDOREDUCTASE (NQR) NEARLY IDENTICAL TO NADPH:QUINONE OXIDOREDUCTASE (NQR) GB:AF145234 [ARABIDOPSIS THALIANA]	Reductase
13365	1670	EXONUCLEASE	Nuclease
13366	1671	PECTIN METHYLESTERASE, PUTATIVE SIMILAR TO PECTIN METHYLESTERASE GB:AAB38794 FROM [LYCOPERSICON ESCULENTUM]	Esterase
13372	1672	PROTEIN KINASE DOMAIN LRR	Kinase, Protein
13385	1673	NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE SIMILAR TO GB:S65812 FROM [ARABIDOPSIS THALIANA] AND OTHER PUTATIVE NON-LTR REVERSE TRANSCRIPTASES	Transcriptase
13389	1674	PEROXIDASE, PUTATIVE SIMILAR TO PEROXIDASE ATP26A GB:CAA72487 GI:1890317 [ARABIDOPSIS THALIANA]	Oxidase

13394	1675	BETA-1,3 GLUCANASE GB:CAB85903 GI:7414433 [PISUM SATIVUM][HYPOTHETICAL PROTEIN SIMILAR TO]	Glycosylase
13417	1676	RECEPTOR KINASE, PUTATIVE SIMILAR TO RECEPTOR KINASE GB:AAD02501 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
13420	1677	PROLYL 4-HYDROXYLASE, PUTATIVE SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 FROM [CAENORHABDITIS ELEGANS]	Hydroxylase
13421	1678	PROLYL 4-HYDROXYLASE, PUTATIVE SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 FROM [CAENORHABDITIS ELEGANS]	Hydroxylase
13424	1679	AAA-TYPE ATPASE GB:AAD31347 GI:4874284 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN SIMILAR TO][PUTATIVE]	ATPase
13441	1680	PROTEIN KINASE, PUTATIVE SIMILAR TO PROTEIN KINASE APK1A GB:Q06548 FROM [ARABIDOPSIS THALIANA]	Kinase, Protein
13485	1681	PECTINESTERASE SIMILAR TO PECTINESTERASE PRECURSOR GB:Q43043 [PETUNIA INTEGRIFOLIA]; CONTAINS PFAM PROFILE: PF01095 PECTINESTERASE[PUTATIVE]	Esterase
13486	1682	VESICLE TRANSPORT PROTEIN SIMILAR TO V-SNARE ATVTI1A GB:AAF24061 [ARABIDOPSIS THALIANA][PUTATIVE]	Transporter
13487	1683	TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY; SIMILAR TO EPIDERMAL GERMACRENE C SYNTHASE GB: AAC39431 [LYCOPERSICON ESCULENTUM], (+)-DELTA-CADINENE SYNTHASE GB:P93665 [GOSSYPIUM HIRSUTUM][PUTATIVE]	Synthase
13496	1684	TERPENE SYNTHASE-RELATED PROTEIN CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase
13497	1685	CHORISMATE MUTASE IDENTICAL TO CHORISMATE MUTASE GB:Z26519 [ARABIDOPSIS THALIANA]	Mutase

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13502	1686	SHORT-CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE GB:AAF04194 [PISUM SATIVUM]; CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE	Dehydrogenase
13503	1687	SHORT-CHAIN ALCOHOL DEHYDROGENASE, PUTATIVE SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE GB:AAF04194 [PISUM SATIVUM]; CONTAINS PFAM PROFILE: PF00106 SHORT CHAIN DEHYDROGENASE	Dehydrogenase
13519	1688	TERPENE SYNTHASE, PUTATIVE SIMILAR TO TERPENE SYNTHASE GB:CAA72074 FROM [ARABIDOPSIS THALIANA], CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase
13520	1689	FARNESYLTRANTRANSFERASE, PUTATIVE (FRAGMENT) FRAGMENT SIMILAR TO FARNESYLTRANTRANSFERASE PRECURSOR GB:T10452 FROM [SINAPIS ALBA]	Transferases
13521	1690	GERANYLGERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GERANYLGERANYL PYROPHOSPHATE SYNTHASE, CHLOROPLAST PRECURSOR GB:P34802 FROM [ARABIDOPSIS THALIANA]	Synthase
13532	1691	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428 FROM [GENTIANA TRIFLORA]	Transferases
13536	1692	FLAVONOL 3-O-GLUCOSYLTRANSFERASE, PUTATIVE SIMILAR TO FLAVONOL 3-O-GLUCOSYLTRANSFERASE GB:Q43716 FROM [PETUNIA X HYBRIDA]	Transferases
13541	1693	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE GB:BAA74428 [GENTIANA TRIFLORA]	Transferases

13542	1694	ANTHOCYANIN S-AROMATIC ACYLTRANSFERASE, PUTATIVE SIMILAR TO ANTHOCYANIN S-AROMATIC ACYLTRANSFERASE GB:BAA74428 [GENTIANA TRIFLORA]	Transferases
13554	1695	ALPHA/BETA HYDROLASE, PUTATIVE CONTAINS PFAM PROFILE: PF00561 ALPHA/BETA HYDROLASE FOLD	Hydrolase
13563	1696	PHYTOCHELATIN SYNTHETASE GB:CAA07251 FROM [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 117, 1526-1526 (1998)), UNKNOWN PROTEIN SIMILAR TO PUTATIVE	Synthase
13564	1697	NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE GB:AAD22368 FROM [ARABIDOPSIS THALIANA][HYPOTHETICAL PROTEIN CONTAINS SIMILARITY TO][PUTATIVE]	Transcriptase
13576	1698	FRUCTOSE-6-PHOSPHATE 2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE GB:AAF04293, HYPOTHETICAL PROTEIN CONTAINS REGIONS SIMILAR TO	Phosphatase
13584	1699	DEACETYLVINDOLINE 4-O-ACETYLTRANSFERASE, PUTATIVE SIMILAR TO GB: AAC99311 FROM [CATHARANTHUS ROSEUS] (PLANT J. 14 (6), 703-713 (1998))	Transferases
13595	1700	AMINO ACID TRANSPORTER; UNKNOWN PROTEIN CONTAINS PFAM PROFILE: PF01490 TRANSMEMBRANE AMINO ACID TRANSPORTER PROTEIN	Transporter
13612	1701	BETA-MANNAN ENDOHYDROLASE SIMILAR TO (1-4)-BETA-MANNAN ENDOHYDROLASE GB:AAB87859 FROM [LYCOPERSICON ESCULENTUM][PUTATIVE]	Hydrolase
13665	1702	VETISPIRADIENE SYNTHASE, PUTATIVE, 5' PARTIAL SIMILAR TO VETISPIRADIENE SYNTHASE GB:BAB02386 GI:9294376 FROM [ARABIDOPSIS THALIANA]	Synthase
13685	1703	TERPENE SYNTHASE, PUTATIVE CONTAINS PFAM PROFILE: PF01397 TERPENE SYNTHASE FAMILY	Synthase

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13686	1704	GERANYLGERANYL PYROPHOSPHATE SYNTHASE, PUTATIVE SIMILAR TO GB:P34802 FROM [ARABIDOPSIS THALIANA] (PLANT PHYSIOL. 104 (4), 1469-1470 (1994))	Synthase
13695	1705	NON-LTR REVERSE TRANSCRIPTASE, PUTATIVE	Transcriptase
13755	1706	PECTIN METHYLESTERASE [PUTATIVE]	Esterase
13796	1707	PEROXIDASE - LYCOPERSICON ESCULENTUM, PIR:S32768[PUTATIVE]	Oxidase
13824	1708	ARABINOSE KINASE - LIKE PROTEIN PUTATIVE ARABINOSE KINASE ISAI, ARABIDOPSIS THALIANA, EMBL:ATY14404	Kinase
13827	1709	RECEPTOR PROTEIN KINASE -LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE PRK1, LYCOPERSICON ESCULENTUM, PIR:T07865	Kinase, Protein
13834	1710	POLYGALACTURONASE -LIKE PROTEIN POLYGALACTURONASE, MUSKMELON, PIR:T08213	Glycosylase
13835	1711	ALCOHOL DEHYDROGENASE (ATA1)	Dehydrogenases
13858	1712	SUCROSE SYNTHASE -LIKE PROTEIN SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE), ARABIDOPSIS THALINA, SWISSPROT:SUS1_ARATH	Synthase
13866	1713	PECTINESTERASE -LIKE PROTEIN PECTINESTERASE PPE8B PRECURSOR, PRUNUS PERSICA, SWISSPROT:PME_PRUPE	Esterase
13868	1714	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, EQUUS CABALLUS, EMBL:AF097179[PUTATIVE]	Dehydrogenases
13906	1715	AMINE OXIDASE -LIKE PROTEIN AMINE OXIDASE, CANAVALIA LINEATA, EMBL:AF172681	Oxidase
13918	1716	TRANSPORTER-LIKE PROTEIN MULTIDRUG-EFFLUX TRANSPORTER BLT, BACILLUS SUBTILIS, PIR:I39792	Transporter
13919	1717	GLUTATHIONE TRANSFERASE-LIKE PROTEIN GLUTATHIONE TRANSFERASE, PAPAYA, PIR:T09781	Transferases
13921	1718	AMINE OXIDASE, CANAVALIA LINEATA, EMBL:AF172681[PUTATIVE]	Oxidase
13991	1719	TRIACYLGLYCEROL LIPASE, PSYCHROBACTER IMMOBILIS, PIR:S57275[PUTATIVE]	Lipase

14001	1720	TYROSINE-PHOSPHATASE-LIKE PROTEIN PROTEIN- TYROSINE-PHOSPHATASE - SCHIZOSACCHAROMYCES POMBE, PIR:A55446	Phosphatase
14011	1721	PREPHENATE DEHYDRATASE CHLOROPLAST SIMILAR TO BACTERIAL PHEA GENE PRODUCTS[PUTATIVE]	Dehydratase
14014	1722	HISTONE DEACETYLASE SIMILAR TO MAIZE NUCLEOLAR HISTONE DEACETYLASE (U82815) [PUTATIVE]	
14022	1723	PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE (EC 2.3.1.43) PRECURSOR, MOUSE, PIR:XXMSN[PUTATIVE]	O-Transferases
14023	1724	PROTEINKINASE ATPP -LIKE PROTEIN ATPP PROTEIN, BRASSICA NAPUS, EMBL:BNA245479	Kinase, Protein
14029	1725	MEMBRANE ION ANTIPORTER, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE]	Transporter
14030	1726	MEMBRANE ION ANTIPORTER, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE]	Transporter
14031	1727	MEMBRANE ION ANTIPORTER, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE]	Transporter
14032	1728	MEMBRANE ION ANTIPORTER, AMYCOLATOPSIS ORIENTALIS, EMBL:AL078635[PUTATIVE]	Transporter
14038	1729	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE	Glycosylase
14045	1730	HIGH-AFFINITY NITRATE TRANSPORTER - LIKE PROTEIN HIGH-AFFINITY NITRATE TRANSPORTER ACHI, ARABIDOPSIS THALIANA, EMBL:AF019748	Transporter
14048	1731	2-PHOSPHOGLYCERATE KINASE - METHANOCOCCUS JANNASCHII, PIR:A64485[PUTATIVE]	Kinase
14072	1732	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
14078	1733	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein

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14080	1734	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
14081	1735	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
14082	1736	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
14083	1737	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE LRK1 - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
14098	1738	TRNA INTRON ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:AB036339[PUTATIVE]	Nuclease
14104	1739	TRANSPORTER PROTEIN[PUTATIVE]	Transporter
14105	1740	TRANSPORTER PROTEIN[PUTATIVE]	Transporter
14106	1741	PROTEIN KINASE NPK1-RELATED PROTEIN KINASE 2 - ARABIDOPSIS THALIANA, EMBL:AB000798[PUTATIVE]	Kinase, Protein
14107	1742	TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE]	Transporter
14108	1743	TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE]	Transporter
14109	1744	TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE]	Transporter
14110	1745	TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE]	Transporter
14111	1746	TRANSPORTER PROTEIN PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, PIR:T04378[PUTATIVE]	Transporter
14118	1747	MAP3K ALPHA 1 PROTEIN KINASE - BRASSICA NAPUS, EMBL:BNA010091[PUTATIVE]	Kinase, Protein

14125	1748	PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE RLK3, ARABIDOPSIS THALIANA, EMBL:ATH011674	Kinase, Protein
14131	1749	PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE HOMOLOG, ARABIDOPSIS THALIANA, PIR:T45691	Kinase, Protein
14149	1750	HISTIDYL-TRNA SYNTHETASE	Synthase
14151	1751	PURPLE ACID PHOSPHATASE PRECURSOR -LIKE PROTEIN PURPLE ACID PHOSPHATASE PRECURSOR PAP1, IPOMOEA BATATAS, EMBL:AF200825	Phosphatase
14153	1752	PROTEIN KINASE - LIKE MEK KINASE ALPHA, DICTYOSTELIUM DISCOIDEUM, EMBL:AF093689	Kinase, Protein
14155	1753	PROTEIN KINASE -LIKE NPK1-RELATED PROTEIN KINASE 2 ANP2, ARABIDOPSIS THALIANA, EMBL:AB000798	Kinase, Protein
14156	1754	DEHYDROGENASE -LIKE PROTEIN ALCOHOL DEHYDROGENASE HOMOLOG, RIPENING-RELATED, TOMATO, PIR:S39508	Dehydrogenases
14163	1755	SERINE/THREONINE-SPECIFIC PROTEIN KINASE (EC 2.7.1.-) LRRPK, ARABIDOPSIS THALIANA, PIR:T08975[PUTATIVE]	Kinase, Protein
14164	1756	PROTEIN (FRAGMENT) SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE]	Kinase, Protein
14165	1757	PROTEIN (FRAGMENT) SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE]	Kinase, Protein
14166	1758	SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE]	Kinase, Protein
14167	1759	SERINE/THREONINE-SPECIFIC PROTEIN KINASE (EC 2.7.1.-) LRRPK, ARABIDOPSIS THALIANA, PIR:T08975[PUTATIVE]	Kinase, Protein
14168	1760	RECEPTOR PROTEIN KINASE -LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060	Kinase, Protein

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14172	1761	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RECEPTOR-LIKE PROTEIN KINASE - CATHARANTHUS ROSEUS, EMBL:Z73295	Kinase, Protein
14173	1762	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE ARABIDOPSIS THALIANA, PIR:S71277	Kinase, Protein
14174	1763	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE ARABIDOPSIS THALIANA, PIR:S71277	Kinase, Protein
14176	1764	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE ARABIDOPSIS THALIANA, PIR:S71277	Kinase, Protein
14179	1765	LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE ARABIDOPSIS THALIANA, PIR:S71277[PUTATIVE]	Kinase, Protein
14188	1766	GIBBERELLIN 20-OXIDASE, SEVERAL OXIDASES, MAINLY [PUTATIVE]	Oxidase
14189	1767	GIBBERELLIN 20-OXIDASE, SEVERAL OXIDASES, MAINLY [PUTATIVE]	Oxidase
14196	1768	GLUCOSIDASE-LIKE PROTEIN GLUCAN ENDO-1,3- BETA-GLUCOSIDASE PRECURSOR - TRITICUM AESTIVUM, SWISSPROT:E13B_WHEAT	Glycosylase
14204	1769	GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819	Transferases
14205	1770	GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819	Transferases
14206	1771	GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819	Transferases
14207	1772	GLUCOSYLTRANSFERASE-LIKE PROTEIN UDP- GLUCOSE GLUCOSYLTRANSFERASE - ARABIDOPSIS THALIANA, EMBL:AB016819	Transferases

14208	1773	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED LYCOPERSICON ESCULENTUM, PIR2:S39507	Transferases
14209	1774	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED LYCOPERSICON ESCULENTUM, PIR2:S39507	Transferases
14211	1775	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED LYCOPERSICON ESCULENTUM, PIR2:S39507	Transferases
14213	1776	CHLOROPLAST IMPORT-ASSOCIATED CHANNEL PROTEIN HOMOLOG CHLOROPLAST IMPORT- ASSOCIATED CHANNEL IAP75 - PISUM SATIVUM, PIR2:S55344	Channel
14215	1777	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, PID:E1188577	Kinase, Protein
14223	1778	SUBTILISIN-LIKE PROTEINASE CUCUMISIN (SERINE PROTEASE, EC 3.4.21.25) PRECURSOR - CUCUMIS MELO, PIR2:A55800	Protease
14224	1779	SUBTILISIN-LIKE PROTEINASE CUCUMISIN (SERINE PROTEASE, EC 3.4.21.25) PRECURSOR - CUCUMIS MELO, PIR2:A55800	Protease
14229	1780	COPPER TRANSPORT PROTEIN - LIKE PROTEIN COPPER TRANSPORTER PROTEIN ARABIDOPSIS THALIANA, PID:G1082054	Transporter
14239	1781	BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1	Hydrolase
14240	1782	BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1	Hydrolase
14243	1783	BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1	Hydrolase

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14244	1784	BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, TREMBL:AB017502_1	Hydrolase
14248	1785	RECEPTOR KINASE-LIKE PROTEIN RECEPTOR KINASE- LIKE PROTEIN (XA21), ORYZA LONGISTAMINATA, U72725	Kinase, Protein
14250	1786	RECEPTOR PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE XA21 RECEPTOR TYPE PRECURSOR, ORYZA SATIVA, PIR:A57676	Kinase, Protein
14258	1787	1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE - LIKE PROTEIN ACC OXIDASE, BRASSICA OLERACEA, X81628	Oxidase
14274	1788	11BETA-HYDROXYSTEROID DEHYDROGENASE - HOMO SAPIENS, PIR1:DXHUBH[PUTATIVE]	Dehydrogenases
14275	1789	11BETA-HYDROXYSTEROID DEHYDROGENASE - RATTUS NORVEGICUS, PIR1:DXRTBH[PUTATIVE]	Dehydrogenases
14277	1790	PECTINESTERASE HOMOLOG - PINUS RADIATA, PIR2:T08112[PUTATIVE]	Esterase
14279	1791	PECTINESTERASE-LIKE PROTEIN PECTINESTERASE (EC 3.1.1.11) - CITRUS SINENSIS, PID:G2098709	Esterase
14284	1792	NITRIC OXIDE SYNTHASE, PROTEIN BR-1 PROTEIN - HELIX POMATIA, PID:E234055[PUTATIVE]	Synthase
14293	1793	ENDOCHITINASE-LIKE PROTEIN BASIC ENDOCHITINASE CHB4 PRECURSOR - BRASSICA NAPUS, SWISSPROT:CHI4_BRANA	Chitinase
14297	1794	RECEPTOR KINASE-LIKE PROTEIN PROTEIN KINASE XA21 - ORYZA SATIVA, PIR:A57676	Kinase, Protein
14306	1795	PECTINESTERASE - ARABIDOPSIS THALIANA, PIR:S51370[PUTATIVE]	Esterase
14318	1796	ABC-TYPE TRANSPORT PROTEIN-LIKE PROTEIN ATP BINDING CASSETTE TRANSPORTER ABC2, HOMO SAPIENS ,PIR2:B54774	Transporter
14334	1797	PEPTIDE TRANSPORTER PEPTIDE TRANSPORTER (PTR1), HORDEUM VULGARE, AF023472[PUTATIVE]	Transporter

14339	1798	CYCLIC NUCLEOTIDE-GATED CHANNEL CYCLIC NUCLEOTIDE-GATED CATION CHANNEL, ARABIDOPSIS THALIANA, AF067798[PUTATIVE]	Channel
14349	1799	GLYCINE-TRNA LIGASE PRECURSOR, CHLOROPLAST (EDD1)	Ligase
14371	1800	LIPASE - LIKE PROTEIN LIPASE ARAB-1, ARABIDOPSIS THALIANA, PIR2:S68410	Lipase
14378	1801	DEOXYCYTIDYLATE DEAMINASE - HOMO SAPIENS, PIR:I55434[PUTATIVE]	Deaminase
14382	1802	ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN EXGT1 (ENDOXYLOGLUCAN TRANSFERASE) - PISUM SATIVUM, EMBL:AB015428	Transferases
14397	1803	GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE	Transferases
14407	1804	POLY A POLYMERASE, C-TERMINUS POLYADENYLATE-BINDING PROTEINS[PUTATIVE]	Polymerase
14419	1805	ENDO-POLYGALACTURONASE - LIKE PROTEIN ENDO POLYGALACTURONASE, ARABIDOPSIS THALIANA, GB:CAA05525	Glycosylase
14424	1806	RNA POLYMERASE III SUBUNIT - LIKE PROTEIN RNA POLYMERASE III SUBUNIT, HOMO SAPIENS, GB:CAB41919	Polymerase
14435	1807	PEROXIDASE	Oxidase
14436	1808	PEROXIDASE	Oxidase
14440	1809	PYRUVATE KINASE -LIKE PROTEIN VARIOUS PYRUVATE KINASES FROM PROCARYOTES	Kinase
14446	1810	PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, CITRUS SINENSIS, GB:AAB57670	Esterase
14455	1811	SUGAR TRANSPORTER 2, DROSOPHILA MELANOGASTER, EMBL:AF199484[PUTATIVE]	Transporter
14460	1812	6-PHOSPHOGLUCONOLACTONASE - LIKE PROTEIN 6-PHOSPHOGLUCONOLACTONASE (6PGL), HOMO SAPIENS, EMBL:HSA243972	LACTONASE
14491	1813	RECEPTOR PROTEIN KINASE - LIKE PROTEIN CLAVATA1 RECEPTOR KINASE, ARABIDOPSIS THALIANA, EMBL:ATU96879	Kinase, Protein
14520	1814	PEROXIDASE ATP21A	Oxidase

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14545	1815	FLAVONOL SYNTHASE - LIKE PROTEIN SRG1 PROTEIN, ARABIDOPSIS THALIANA, PIR:S44261	Synthase
14547	1816	RECEPTOR PROTEIN KINASE -LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE (RKL1), ARABIDOPSIS THALIANA, EMBL:AF084034	Kinase, Protein
14551	1817	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS	N-Transferases
14552	1818	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10717	N-Transferases
14553	1819	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10711[PUTATIVE]	N-Transferases
14554	1820	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE LIKE PROTEIN ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10719	N-Transferases
14563	1821	MYOSIN HEAVY CHAIN KINASE B, DICTYOSTELIUM DISCOIDEUM, GB:U90946[PUTATIVE]	Kinase, Protein
14573	1822	REVERSE TRANSCRIPTASE FRAGMENTS[PUTATIVE]	Transcriptase
14576	1823	PHOSPHOGLYCERATE MUTASES[PUTATIVE]	Mutase
14580	1824	STEROID DEHYDROGENASE HOMOLOG - HOMO SAPIENS, EMBL:AF078850[PUTATIVE]	Dehydrogenase
14598	1825	UTP-GLUCOSE GLUCOSYLTRANSFERASE - LIKE PROTEIN UTP-GLUCOSE GLUCOSYLTRANSFERASE, MANIHOT ESCULENTA, PIR:S41951	Transferases
14600	1826	UDP-GLUCOSE:(GLUCOSYL) GLUCOSYLTRANSFERASE LPS WAAO, ALPHA1,3- E.COLI, EMBL:AF019746[PUTATIVE]	Transferases

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14623	1827	PEROXIDASE-LIKE PROTEIN PEROXIDASE ATP6A ARABIODOPSIS THALIANA, EMBL:X98774	Oxidase
14645	1828	STEROID SULFOTRANSFERASE 2 - BRASSICA NAPUS, EMBL:AF000306[PUTATIVE]	Transferases
14648	1829	FLAVANONE 3-HYDROXYLASE (FH3)	Hydroxylase
14661	1830	PROTEIN PHOSPHATASE 2C -LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF097667	Phosphatase
14671	1831	PROTEIN PHOSPHATASE 2C-LIKE PROTEIN PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF075580	Phosphatase
14672	1832	GLUTAMATE RECEPTOR PUTATIVE GLUTAMATE RECEPTOR GLR2, ARABIDOPSIS THALIANA, EMBL:AF079999[PUTATIVE]	Receptor
14673	1833	SUGAR TRANSPORTER-LIKE PROTEIN SUGAR TRANSPORTER, ARABIDOPSIS THALIANA, EMBL:Z50752	Transporter
14679	1834	RECEPTOR-PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, CATHARANTHUS ROSEUS, PIR:T10060	Kinase, Protein
14692	1835	SHORT-CHAIN ALCOHOL DEHYDROGENASE-LIKE PROTEIN SHORT-CHAIN ALCOHOL DEHYDROGENASE - ZEA MAYS, PIR:A47542	Dehydrogenase
14695	1836	PROTEIN KINASE PK1, RECEPTOR-LIKE - ZEA MAYS, PIR:S33532[PUTATIVE]	Kinase, Protein
14706	1837	CHLOROPHYLL SYNTHETASE	Synthase
14710	1838	CA2+/H+-EXCHANGING PROTEIN-LIKE ARABIDOPSIS THALIANA HIGH AFFINITY CALCIUM ANTIPORTER CAX1 ENCODED BY GENBANK ACCESSION NUMBER U57411	Transporter
14717	1839	MYOSIN HEAVY CHAIN KINASE B - DICTYOSTELIUM DISCOIDEUM, PID:G1903458[PUTATIVE]	Kinase, Protein
14721	1840	WAX SYNTHASE-LIKE PROTEIN WAX SYNTHASE - SIMMONDSIA CHINENSIS, PID:G5020219	Synthase
14729	1841	DNA POLYMERASE I -BACILLUS STEAROTHERMOPHILUS, PIR2:S70368[PUTATIVE]	Polymerase

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14740	1842	BETA-KETOACYL-COA SYNTHASE LIKE PROTEIN BETA-KETOACYL-COA SYNTHASE - SIMMONDSIA CHINENSIS,PID:G1045614	Synthase
14750	1843	PSEUDOURIDINE SYNTHASE, PUTATIVE SIMILAR TO RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE,D,SP:P33643 [ESCHERICHIA COLI]	Synthase
14777	1844	PROTEIN KINASE-LIKE PROTEIN - ARABIDOPSIS THALIANA (F15B8.110),PIR2:T06750[PUTATIVE]	Kinase, Protein
14784	1845	BETA-FRUCTOFURANOSIDASE	Glycosylase
14786	1846	PHOSPHATE ACTYLTRANSFERASE, STAPHYLOCOCCUS AUREUS, EMBL:SAU271496[PUTATIVE]	Transferases
14796	1847	CARBONIC ANHYDRASE (CAH1)	Anhydrase
14802	1848	PURPLE ACID PHOSPHATASE-LIKE PROTEIN PURPLE ACID PHOSPHATASE PRECURSOR, PHASEOLUS VULGARIS, EMBL:PVPAPHOSP	Phosphatase
14809	1849	VACUOLAR SORTING RECEPTOR HOMOLOG/ATELPI and SPOT 3 PROTEIN	Receptor
14812	1850	MONODEHYDROASCORBATE REDUCTASE (NADH) - LIKE PROTEIN MONODEHYDROASCORBATE REDUCTASE (NADH), LYCOPERISON ESCULENTUM, PIR:T06407	Reductase
14825	1851	PROTEIN KINASE, ARABIDOPSIS THALIANA[PUTATIVE]	Kinase, Protein
14832	1852	BETA-GALACTOSIDASE PRECURSOR, LYCOPERSICON ESCULENTUM, GB:P48980[PUTATIVE]	Glycosylase
14838	1853	CAFFEIC ACID O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE (HOMT1), POPULUS KITAKAMIENSIS, EMBL:PKHOMT1A	Transferases
14839	1854	GLUCOSYLTRANSFERASE - LIKE PROTEIN GLUCOSYLTRANSFERASE IS10A, SALICYLATE-INDUCED, NICOTIANA TABACUM, PIR:T03745	Transferases
14840	1855	GLUCOSYLTRANSFERASE - LIKE PROTEIN GLUCOSYLTRANSFERASE IS5A, NICOTIANA TABACUM, PIR:T03747	Transferases

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14841	1856	NODULIN / GLUTAMATE-AMMONIA LIGASE - LIKE PROTEIN MTN6, MEDICAGO TRUNCATULA, EMBL:MTY18225	Ligase
14842	1857	NODULIN / GLUTAMATE-AMMONIA LIGASE - LIKE PROTEIN MTN6 - NODULIN 6, MEDICAGO TRUNCATULA, EMBL:MET133118	Ligase
14843	1858	PECTATE LYASE -LIKE PROTEIN PECTATE LYASE, MUSA ACUMINATA, EMBL:MAPEL	Lyase
14851	1859	CLP ENDOPEPTIDASE ATP-BINDING CHAIN C, CHLAMYDIA PNEUMONIAE, PIR:G72079[PUTATIVE]	Protease
14862	1860	RECEPTOR LECTIN KINASE -LIKE PROTEIN RECEPTOR LECTIN KINASE 3, ARABIDOPSIS THALIANA, GB:U93161	Kinase, Protein
14869	1861	LYSINE DECARBOXYLASE (ECORLD), EIKENELLA CORRODENS, EMBL:U89166[PUTATIVE]	Decarboxylase
14882	1862	DIAMINOPIMELATE EPIMERASE - LIKE PROTEIN DIAMINOPIMELATE EPIMERASE, PSEUDOMONAS FLUORESCENS, PIR:T10459	Epimerase
14886	1863	INORGANIC PYROPHOSPHATASE -LIKE PROTEIN INORGANIC PYROPHOSPHATASE, SOLANUM TUBEROSUM, PIR:T07399	Phosphatase
14896	1864	NA(+)/H(+) ANTIPORTER[PUTATIVE]	Transporter
14905	1865	SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN SERINE/THREONINE-SPECIFIC KINASE (EC 2.7.1.-) PRECURSOR - ARABIDOPSIS THALIANA, PIR:S68589	Kinase, Protein
14908	1866	PROTEIN KINASE-LIKE PROTEIN WALL-ASSOCIATED KINASE 4 - ARABIDOPSIS THALIANA, EMBL:ATH9695	Kinase, Protein
14914	1867	URACIL PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN URACIL PHOSPHORIBOSYLTRANSFERASE - NICOTIANA TABACUM, PIR:T03969	Transferases
14915	1868	MALAT DEHYDROGENASE [PUTATIVE]	Dehydrogenase
14919	1869	GLYOXAL OXIDASE (GLX2) - PHANEROCHAETE CHRYSOSPORIUM, EMBL:L47287[PUTATIVE]	Oxidase
14927	1870	PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615	Kinase, Protein

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14933	1871	FRUCTOKINASE - LIKE PROTEIN FRUCTOKINASE, LYCOPERSICON ESCULENTUM, EMBL:LEU62329	Kinase
14948	1872	ESTERASE, PSEUDOMONAS FLUORESCENS, EMBL:PF12537[PUTATIVE], PROTEIN (FRAGMENT)	Esterase
14966	1873	CHITINASE CLASS IV (CHIV)	Chitinase
14969	1874	RNA POLYMERASE 24KDA SUBUNIT -LIKE PROTEIN RNA POLYMERASE SUBUNIT, ARABIDOPSIS THALIANA, EMBL:AF019248	Polymerase
14985	1875	SUGAR-PHOSPHATE ISOMERASE - LIKE PROTEIN GUTQ/KPSF FAMILY SUGAR-P ISOMERASE, CHLAMYDIA PNEUMONIAE, PIR:E72068	Isomerase
14986	1876	PHOSPHATE TRANSPORT PROTEIN PHOSPHATE TRANSPORTER, NICOTIANA TABACUM, EMBL:AB020061	Transporter
14999	1877	VESICULAR TRANSPORTER UNC-47, CAENORHABDITIS ELEGANS, AF031935[PUTATIVE]	Transporter
15008	1878	PECTATE LYASE - LIKE PROTEIN PECTATE LYASE, MUSA ACUMINATA, X92943	Lyase
15019	1879	PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE - LIKE PROTEIN PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE, PSEUDOMONAS FLUORESCENS, EMBL:L29642	Synthase
15021	1880	PROTEIN PHOSPHATASE 2C - LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL AF097667	Phosphatase
15028	1881	CHALCONE ISOMERASE	Isomerase
15034	1882	LIPASE -LIKE PROTEIN MONOGLYCERIDE LIPASE, MUS MUSCULUS, EMBL:MMMGLYLIP	Lipase
15035	1883	LIPASE -LIKE PROTEIN MONOGLYCERIDE LIPASE, MUS MUSCULUS, EMBL:MMMGLYLIP	Lipase
15041	1884	PECTATE-LYASE, ARABIDOPSIS THALIANA, PIR:T06728[PUTATIVE]	Lyase
15043	1885	DUAL SPECIFICITY PROTEIN PHOSPHATASE 5, PHOSPHATASE - LIKE PROTEIN, RATTUS NORWEGICUS, SWISSPROT:DUS5_RAT	Phosphatase

15045	1886	ALCOHOL DEHYDROGENASE HOMOLOG, TOMATO, PIR:S3950811BETA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.146) I - MOUSE, PIR:1:I56604[PUTATIVE] OXIDOREDUCTASE -LIKE PROTEIN RIPENING-RELATED	Dehydrogenases
15047	1887	BETA-KETOACYL-ACP REDUCTASE - LIKE PROTEIN BETA-KETOACYL-ACP REDUCTASE, CUPHEA LANCEOLATA, EMBL:X64566	Reductase
15059	1888	BETA-1,3-GLUCANASE - LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE, TRITICUM AESTIVUM, PIR:T06268	Glycosylase
15061	1889	SERINE/THREONINE-SPECIFIC PROTEIN KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK, ARABIDOPSIS THALIANA, PIR:S38326	Kinase, Protein
15086	1890	GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, LYCOPERSICON ESCULENTUM, PIR:S39507	Transferases
15087	1891	GLUCURONOSYL TRANSFERASE - LIKE PROTEIN GLUCURONOSYL TRANSFERASE HOMOLOG, LYCOPERSICON ESCULENTUM, PIR:S39507	Transferases
15090	1892	PROLINE TRANSPORTER 2	Transporter
15094	1893	BETA-1,3-GLUCANASE - LIKE PROTEIN BETA-1,3-GLUCANASE, ARABIDOPSIS THALIANA, PIR:S31906	Glycosylase
15096	1894	SEDOHEPTULOSE-BISPHTOSPHTASE PRECURSOR	Phosphatase
15103	1895	ANTHRANILATE SYNTHASE ALPHA-1 CHAIN - LIKE PROTEIN ANTHRANILATE SYNTHASE ALPHA SUBUNIT, RUTA GRAVEOLENS, EMBL:RGANTSYNB	Synthase
15111	1896	RECEPTOR KINASE - LIKE PROTEIN RECEPTOR KINASE HOMOLOG CRINKLY4, MAIZE, PIR:T04108	Kinase, Protein
15113	1897	LEUCOANTHOCYANIDIN DIOXYGENASE -LIKE PROTEIN LEUCOANTHOCYANIDIN DIOXYGENASE, APPLE TREE, PIR:S33144	Oxygenases
15116	1898	CELLULOSE SYNTHASE (CELA), AGROBACTERIUM TUMEFACIENS, EMBL:ATCELABC[PUTATIVE]	Synthase

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15121	1899	PROTEIN KINASE SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15 - NICOTIANA TABACUM, PIR:S52578[PUTATIVE]	Kinase, Protein
15122	1900	MANDELONITRILE LYASE-LIKE PROTEIN ADHESION OF CALYX EDGES (ACE) - ARABIDOPSIS THALIANA	Lyase
15129	1901	ACETYL-COA CARBOXYLASE, BIOTIN CARBOXYL CARRIER - ANABAENA SP., PIR:B53311[PUTATIVE]	Carboxylase
15136	1902	GLUTAMINE TRANSPORTER NEURONAL - RATTUS NORVEGICUS, EMBL:AF075704[PUTATIVE]	Transporter
15144	1903	PROTEIN KINASE NPK1-RELATED PROTEIN KINASE 1S - ARABIDOPSIS THALIANA, EMBL:AB000797	Kinase, Protein
15148	1904	POLY(A) POLYMERASE - CANDIDA ALBICANS, EMBL:AB009394[PUTATIVE]	Polymerase
15149	1905	N2,N2-DIMETHYLGUANOSINE METHYLTRANSFERASES-LIKE PROTEIN SEVERAL N2,N2-DIMETHYLGUANOSINE METHYLTRANSFERASES	TRNA Transfases TRNA
15153	1906	LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE - MALUS DOMESTICA, EMBL:AF053127[PUTATIVE]	Kinase, Protein
15162	1907	QUINONE REDUCTASE-LIKE PROTEIN ZETA- CRYSTALLIN / QUINONE REDUCTASE (NADPH) - MUS MUSCULUS, PIR:A54932	Reductase
15200	1908	GLYCEROL-3-PHOSPHATE DEHYDROGENASES - BACTERIA[PUTATIVE]	Dehydrogenases
15224	1909	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE (RPB25) - HOMO SAPIENS, EMBL:J04965[PUTATIVE]	Polymerase
15240	1910	BETA-1,3-GLUCANASE	Glycosylase
15242	1911	BETA-1,3-GLUCANASE 2 (BG2) (PR-2)	Glycosylase
15243	1912	GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE-LIKE PROTEIN GLUCAN ENDO-1,3-BETA-D-GLUCOSIDASE - GLYCINE MAX, PIR:T07108	Glycosylase
15263	1913	METALLOENDOPEPTIDASE NRD2 CONVERTASE - RATTUS SP, EMBL: X93208[PUTATIVE]	Protease
15264	1914	PROTEASE-LIKE PROTEIN INSULIN-DEGRADING ENZYME - RATTUS NORVEGICUS, SWISSPROT:P35559	Protease

15268	1915	ENDO-POLYGALACTURONASE	Glycosylase
15273	1916	ACETYLGLUTAMATE KINASE-LIKE PROTEIN ACETYLGLUTAMATE KINASE - SYNECHOCYSTIS SP., PIR:S77509	Kinase
15279	1917	GALACTOSE OXIDASE PRECURSO, CLADOBOTRYUM DENDROIDES, PIR2:A38084[PUTATIVE]	Oxidase
15281	1918	WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE]	Kinase, Protein
15283	1919	DNA-DIRECTED RNA POLYMERASE I 190K CHAIN - LIKE PROTEIN DNA-DIRECTED RNA POLYMERASE(EC 2.7.7.6) I 190K CHAIN, SACCHAROMYCES CEREVISIAE, PIR2:S67250	Polymerase
15285	1920	CARBOXYL TERMINAL PROTEASE - LIKE PROTEIN CARBOXYL TERMINAL PROTEASE, NOSTOC PUNCTIFORME, AF022823	Protease
15287	1921	WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695	Kinase, Protein
15288	1922	WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695	Kinase, Protein
15289	1923	PROTEIN KINASE - LIKE PROTEIN S-RECEPTOR KINASE (EC 2.7.1.-) PRECURSOR, BRASSICA OLERACEA, PIR1:S31429	Kinase, Protein
15290	1924	WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE]	Kinase, Protein
15291	1925	WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695[PUTATIVE]	Kinase, Protein
15292	1926	WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696	Kinase, Protein
15293	1927	WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, AJ009696[PUTATIVE]	Kinase, Protein
15294	1928	WALL-ASSOCIATED KINASE 4, ARABIDOPSIS THALIANA, AJ009695	Kinase, Protein
15296	1929	POLYGALACTURONASE (EC 3.2.1.15) PRECURSOR, ERWINIA CAROTOVORA, PIR:S11773[PUTATIVE]	Glycosylase
15300	1930	RECEPTOR-LIKE PROTEIN KINASE SEVERAL RECEPTOR-LIKE PROTEIN KINASES	Kinase, Protein

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15305	1931	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE - PISUM SATIVUM, PIR:T06460	Transferases
15327	1932	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR - TRITICUM AESTIVUM, SWISSPROT:P52409[PUTATIVE]	Glycosylase
15366	1933	SPHINGOLIPID TRANSPORT PROTEIN LCB3 - SACCHAROMYCES CEREVISIAE, PIR:S55178[PUTATIVE]	Transporter
15378	1934	KETOL-ACID REDUCTOISOMERASE	Isomerase
15386	1935	SERINE/THREONINE-SPECIFIC PROTEIN KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK, ARABIDOPSIS THALIANA, PIR:S38326	Kinase, Protein
15391	1936	CITRATE SYNTHASE -LIKE PROTEIN CITRATE SYNTHASE, CUCURBIT, PIR:S53007	Synthase
15392	1937	CITRATE SYNTHASE -LIKE PROTEIN CITRATE SYNTHASE, CUCURBIT, PIR:S53007	Synthase
15393	1938	TYROSINE KINASE, DICTYOSTELIUM DISCOIDEUM, PIR:A35670[PUTATIVE]	Kinase, Protein
15399	1939	RIBOSOMAL RNA APURINIC SITE SPECIFIC LYASE, TRITICUM AESTIVUM, EMBL:AB032123[PUTATIVE]	Lyase
15416	1940	3-ISOPROPYLMALATE DEHYDRATASE-LIKE PROTEIN (SMALL SUBUNIT) 3-ISOPROPYLMALATE DEHYDRATASE, SMALL SUBUNIT - THERMOTOGA MARITIMA, PIR:A72363	Dehydratase
15418	1941	PECTINESTERASE PRECURSOR-LIKE PROTEIN PECTINESTERASE (EC 3.1.1.11) PRECURSOR - PISUM SATIVUM, PIR:T06468	Esterase
15427	1942	CALLOSE SYNTHASE CATALYTIC SUBUNIT (CFL1) - GOSSYPIUM HIRSUTUM, EMBL:AF085717[PUTATIVE]	Synthase
15428	1943	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE (RKS2) - ARABIDOPSIS THALIANA, EMBL:AF084036	Kinase, Protein
15431	1944	ABC TRANSPORTER-LIKE PROTEIN PUTATIVE MULTI RESISTANCE PROTEIN MRP - ARABIDOPSIS THALIANA, EMBL:ATMRPPROT	Transporter

15452	1945	PROTEIN KINASE-LIKE PROTEIN PTO KINASE INTERACTOR 1 - LYCOPERSICON ESCULENTUM, EMBL:U28007	Kinase, Protein
15453	1946	TRANSPORTER-LIKE PROTEIN UDP-GALACTOSE TRANSPORT PROTEIN HOMOLOG SCHIZOSACCHAROMYCES POMBE, PIR:T43506	Transporter
15459	1947	RECEPTOR KINASE HOMOLOG CRINKLY4 - ZEA MAYS, PIR:T04108[PUTATIVE]	Kinase, Protein
15465	1948	FRUCTOKINASE-LIKE PROTEIN FRUCTOKINASE LYCOPERSICON ESCULENTUM, EMBL:LEU62329	Kinase
15487	1949	SERINE/THREONINE-SPECIFIC KINASE LECRK1 PRECURSOR,LECTIN RECEPTOR-LIKE	Kinase, Protein
15490	1950	RECEPTOR LECTIN KINASE-LIKE PROTEIN (FRAGMENT) RECEPTOR LECTIN KINASE 3 ARABIDOPSIS THALIANA, EMBL:U93161	Kinase, Protein
15491	1951	RECEPTOR LECTIN KINASE 3	Kinase, Protein
15492	1952	RECEPTOR LECTIN KINASE-LIKE PROTEIN RECEPTOR LECTIN KINASE 3 - ARABIDOPSIS THALIANA, EMBL:U93161	Kinase, Protein
15500	1953	SERINE/THREONINE-PROTEIN KINASE CTR1 ARABIDOPSIS THALIANA, EMBL:L08789[PUTATIVE]	Kinase, Protein
15502	1954	POLYGALACTURONASE-LIKE PROTEIN POLYGALACTURONASE - PRUNUS PERSICA, PIR:S40123	Glycosylase
15506	1955	DIHYDRODIPICOLINATE REDUCTASES (DAPB)[PUTATIVE]	Reductase
15579	1956	PHOSPHATIDATE CYTIDYLTRANSFERASE - LIKE PROTEIN PHOSPHATIDATE CYTIDYLTRANSFERASE, SYNECHOCYSTIS SP., PIR:S77254	Transferases
15590	1957	PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, SWEET ORANGE, PIR:T10494	Esterase
15605	1958	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR	Synthase
15612	1959	APURINIC ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:X76912 (AT C-TERMINUS)[PUTATIVE]	Nuclease
15620	1960	APURINIC ENDONUCLEASE - ARABIDOPSIS THALIANA, EMBL:X76912 (AT C-TERMINUS)[PUTATIVE]	Nuclease

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15647	1961	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN PHOSPHORIBOSYLTRANSFERASE PISUM SATIVUM, PIR:T06460	ANTHRANILATE (FRAGMENT)	Transfases
15657	1962	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE-LIKE PROTEIN 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG - ARABIDOPSIS THALIANA, PIR:S59548	Oxidase	
15658	1963	PROTEIN KINASE HOMOLOG F4I18.11 - ARABIDOPSIS THALIANA, PIR:T02456[PUTATIVE]	Kinase, Protein	
15666	1964	POLYGALACTURONASE - EMBL:ZMPGAL3[PUTATIVE]	ZEA MAYS,	Glycosylase
15670	1965	3-METHYL-2-OXOBUTANOATE HYDROXY-METHYL TRANSFERASE-LIKE PROTEIN HYDROXYMETHYLTRANSFERASE - NIDULANS, EMBL:AF134703	KETOPANTOATE - EMERICELLA	Transfases
15671	1966	PROLYL AMINOPEPTIDASE-LIKE PROTEIN PROLYL AMINOPEPTIDASE - AEROMONAS SOBRIA, PIR:JC4184	PROLYL AMINOPEPTIDASE - AEROMONAS SOBRIA, PIR:JC4184	Protease
15689	1967	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PISUM SATIVUM, EMBL:D86180[PUTATIVE]	-	Transfases
15698	1968	BETA-1,3-GLUCANASE PRECURSOR - ORYZA SATIVA, EMBL:U72255[PUTATIVE]	-	Glycosylase
15716	1969	O-METHYLTRANSFERASE - DIFFERENT SPECIES[PUTATIVE]	-	Transfases
15723	1970	PECTINACETYLESTERASE PRECURSOR-LIKE PROTEIN PECTINACETYLESTERASE PRECURSOR - VIGNA RADIATA, EMBL:X99348	-	Esterase
15728	1971	POLYGALACTURONASE - LYCOPERSICON ESCULENTUM, EMBL:AF118567[PUTATIVE]	-	Glycosylase
15730	1972	ISOPENICILLIN N EPIMERASE - STREPTOMYCES CLAVULIGERUS, EMBL:M32324[PUTATIVE]	-	Epimerase
15733	1973	10-DEACETYLBACCATIN III-10-O-ACETYL TRANSFERASE - TAXUS CUSPIDATA, EMBL:AF193765[PUTATIVE]	-	Transfases
15734	1974	PECTINESTERASE-LIKE PROTEIN PECTINESTERASE - BRASSICA RAPA, EMBL:L48178	-	Esterase

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15735	1975	PECTIN METHYLESTERASE - ARABIDOPSIS THALIANA, EMBL:AJ250430[PUTATIVE]	Esterase
15768	1976	protein DISULFIDE-ISOMERASE - ZEA MAYS, PIR:S69181[PUTATIVE]	Isomerase
15782	1977	MITOCHONDRIAL CARRIER PROTEIN AT2G47490 - ARABIDOPSIS THALIANA, EMBL:AC002535[PUTATIVE]	Transporter
15783	1978	GLYCOSYL TRANSFERASE LGTC - NEISSERIA GONORRHOEAE, EMBL:AF208062[PUTATIVE]	Transferases
15787	1979	ABC TRANSPORTER-LIKE PROTEIN GLUTATHIONE CONJUGATE TRANSPORTER ATMRP4 - ARABIDOPSIS THALIANA, EMBL:AJ002584	Transporter
15788	1980	BETA-D-GLUCAN EXHYDROLASE-LIKE PROTEIN EXHYDROLASE II - ZEA MAYS, EMBL:AF064707	Hydrolase
15789	1981	ALPHA GALACTOSYLTTRANSFERASE-LIKE PROTEIN ALPHA GALACTOSYLTTRANSFERASE - TRIGONELLA FOENUM-GRAECUM, EMBL:TFO245478	Transferases
15793	1982	GLUTATHIONE TRANSFERASE III-LIKE PROTEIN GLUTATHIONE TRANSFERASE III(B) - ZEA MAYS, EMBL:AJ010296	Transferases
15799	1983	PECTINESTERASE HOMOLOG - PINUS RADIATA, PIR:T08112[PUTATIVE]	Esterase
15803	1984	LYSOPHOSPHOLIPASE HOMOLOG - ORYZA SATIVA, PIR:T02661[PUTATIVE]	Lipase
15805	1985	AMINO ACID SELECTIVE CHANNEL PROTEIN HORDEUM VULGARE, EMBL:AJ011921[PUTATIVE]	Channel
15828	1986	TRNA ISOPENTENYL TRANSFERASE-LIKE PROTEIN TRNA ISOPENTENYL TRANSFERASE, ARABIDOPSIS THALIANA, EMBL:AF109376	Transferases
15845	1987	SERINE/THREONINE-PROTEIN KINASE NEK4 - MUS MUSCULUS, EMBL:AF099067[PUTATIVE]	Kinase, Protein
15849	1988	PROTEIN PHOSPHATASE 2C - RATTUS NORVEGICUS, EMBL:AF095927[PUTATIVE]	Phosphatase
15850	1989	MAP KINASE [PUTATIVE]	Kinase, Protein
15851	1990	PROTEIN PHOSPHATASE 2C - RATTUS NORVEGICUS, EMBL:AF095927[PUTATIVE]	Phosphatase

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15861	1991	CYTOKININ OXIDASE -LIKE PROTEIN CYTOKININ OXIDASE, ZEA MAYS, EMBL:ZMY18377	Oxidase
15873	1992	CHALCONE SYNTHASE SIMILAR TO PLANT CHALCONE AND STILBENE SYNTHASES[PUTATIVE]	Synthase
15880	1993	NUCLEOTIDE SUGAR EPIMERASE [PUTATIVE]	Epimerase
15888	1994	PECTINESTERASE [PUTATIVE]	Esterase
15892	1995	CUCUMISIN PROTEASE [PUTATIVE]	Protease
15893	1996	PHOSPHOLIPASE D-LIKE PROTEIN	Lipase
15897	1997	LIGHT REPRESSIBLE RECEPTOR PROTEIN KINASE (PID:E242366), SIMILAR TO A. THALIANA	Kinase, Protein
15903	1998	S-DOMAIN RECEPTOR-LIKE PROTEIN KINASE, ZEA MAYS, SIMILARITY TO	Kinase, Protein
15918	1999	BETA-AMYLASE SIMILAR TO THE FAMILY OF GLYCOSYL HYDROLASES[PUTATIVE]	Hydrolase
15921	2000	ACETYL COA THIOESTERASE [PUTATIVE]	Esterase
15925	2001	DTDP-6-DEOXY-L-MANNOSE-DEHYDROGENASE [PUTATIVE]	Dehydrogenases
15932	2002	POTASSIUM/H ⁺ ANTIPORTER [PUTATIVE]	Transporter
15939	2003	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE [PUTATIVE]	Transferases
15970	2004	CYCLIC NUCLEOTIDE GATED CHANNEL (CNGC4) LIKE PROTEIN ARABIDOPSIS THALIANA CYCLIC NUCLEOTIDE GATED CHANNEL (CNGC4), PID:G4378659	Channel
15976	2005	FLAVONOL GLUCOSYLTRANSFERASE SIMILAR TO MANIHOT ESCULENTA FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5, GENBANK ACCESSION NUMBER Q40287[PUTATIVE]	Transferases
15982	2006	ACETYLTRANSFERASE SIMILAR TO DIGITALIS LANATA LANATOSIDE 15'-O-ACETYLTRANSFERASE, GENBANK ACCESSION NUMBER AJ011567[PUTATIVE]	Transferases
16002	2007	PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16011	2008	CALCIUM-REGULATED PROTEIN PHOSPHATASE SIMILAR TO N. CRASSA CALCINEURIN CALCIUM-REGULATED PROTEIN PHOSPHATASE, GENBANK ACCESSION NUMBER P87072[PUTATIVE]	Phosphatase
16016	2009	WATER CHANNEL PROTEIN [PUTATIVE]	Channel

16017	2010	INORGANIC PHOSPHATASE [PUTATIVE]	Phosphatase
16022	2011	REVERSE TRANSCRIPTASE-LIKE PROTEIN [PUTATIVE]	Transcriptase
16037	2012	PROTOPORPHYRINOGEN OXIDASE	Oxidase
16038	2013	CHITINASE SIMILAR TO PEANUT TYPE II CHITINASE, GENBANK ACCESSION NUMBER X82329, E.C. 3.2.1.14[PUTATIVE]	Chitinase
16048	2014	SECA-TYPE CHLOROPLAST PROTEIN TRANSPORT FACTOR [PUTATIVE]	Transporter
16049	2015	PROTEIN TRANSPORT FACTOR [PUTATIVE]	Transporter
16052	2016	POTASSIUM CHANNEL [PUTATIVE]	Channel
16065	2017	RAFFINOSE SYNTHASE OR SEED IMBIBITION PROTEIN SIMILAR TO CUCUMBER RAFFINOSE SYNTHASE, GENBANK ACCESSION NUMBER AF073744[PUTATIVE]	Synthase
16069	2018	NAK-LIKE SER/THR PROTEIN KINASE SIMILAR TO A. THALIANA NAK SER/THR PROTEIN KINASE, GENBANK ACCESSION NUMBER P43293[PUTATIVE]	Kinase, Protein
16081	2019	GLYCOSYL TRANSFERASE SIMILAR TO LGTC OF NEISSERIA SP., GENBANK ACCESSION NUMBER U14554, SIMILAR TO LGTC, GENBANK ACCESSION NUMBER U65788	Transferases
16094	2020	GTP PYROPHOSPHOKINASE SIMILAR TO BACTERIAL GTP PYROPHOSPHOKINASES (RELA) SIMILAR TO B. SUBTILIS RELA (EC 2.7.6.5), GENBANK ACCESSION NUMBER 2635224 CARBOXYL REGION OF PROTEIN NOT DEFINED[PUTATIVE]	Kinase
16096	2021	SUCROSE SYNTHETASE SIMILAR TO SEVERAL PLANT SUGAR SYNTHETASES SIMILAR TO P. SATIVUM SECOND SUGAR SYNTHETASE, GENBANK ACCESSION NUMBER AJ001071 SIMILAR TO BEET SUCROSE SYNTHETASE (EC 2.4.1.13), GENBANK ACCESSION NUMBER S71494[PUTATIVE]	Synthase
16098	2022	PECTINESTERASE SIMILAR TO SEVERAL PLANT PECTINESTERASES[PUTATIVE]	Esterase
16100	2023	PECTINESTERASE - LIKE PROTEIN SIMILAR TO BACTERIAL AND FUNGI PECTINESTERASES	Esterase

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16101	2024	PECTINESTERASE, SIMILAR TO	Esterase
16118	2025	GLYCOSYLTRANSFERASE SIMILAR TO A. THALIANA PROTEIN T20K9.11, GENBANK ACCESSION NUMBER 3445207[PUTATIVE]	Transferases
16120	2026	GLUTATHIONE S TRANSFERASE, ATPM24.1	Transferases
16129	2027	TRYPTOPHAN SYNTHASE ALPHA 1-LIKE PROTEIN SIMILAR TO A. THALIANA TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20), GENBANK ACCESSION NUMBER U18993	Synthase
16131	2028	SERINE/THREONINE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16137	2029	Glutamate N-METHYL-D-ASPARTATE RECEPTOR; GLUTAMATE-/ASPARTATE-BINDING PEPTIDE SIMILAR TO RAT N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN, GENBANK ACCESSION NUMBER S19586[PUTATIVE]	Receptor
16146	2030	ENT-KAURENE SYNTHETASE A - LIKE PROTEIN	Synthase
16173	2031	OXIDOREDUCTASE SIMILAR TO A. THALIANA PUTATIVE PROTEIN F21P8.230, GENBANK ACCESSION NUMBER 3445238[PUTATIVE]	Reductase
16174	2032	GIBBERELLIN 20-OXIDASE, GENBANK ACCESSION NUMBER U70530[PUTATIVE], OXIDOREDUCTASE SIMILAR TO P. VULGARIS	Oxidase
16175	2033	OXIDOREDUCTASE [PUTATIVE]	Reductase
16182	2034	ALCOHOL DEHYDROGENASE SIMILAR TO PLANT SHORT CHAIN ALCOHOL DEHYDROGENASE[PUTATIVE]	Dehydrogenases
16189	2035	XYLOGLUCAN ENDOTRANSGLYCOSYLASE [PUTATIVE]	Glycosylase
16191	2036	RECEPTOR KINASE [PUTATIVE]	Kinase, Protein
16194	2037	PROTEIN PHOSPHATASE REGULATORY SUBUNIT [PUTATIVE]	Phosphatase
16202	2038	GLYCOSYLATION ENZYME SIMILAR TO B. TAURUS CORE2-GLCNAC-TRANSFERASE, GENBANK ACCESSION NUMBER U41320[PUTATIVE]	Transferases

16207	2039	LRR RECEPTOR-LIKE PROTEIN KINASE SIMILAR TO Z MAYS LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN KINASE LRRTPK 1, GENBANK ACCESSION NUMBER AF023164[PUTATIVE]	Kinase, Protein
16221	2040	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
16223	2041	GLUCAN SYNTHASE COMPONENT SIMILAR TO 1,3-BETA GLUCAN SYNTHASE[PUTATIVE]	Synthase
16229	2042	HYDROLASE [PUTATIVE]	Hydrolase
16261	2043	PECTINESTERASE [PUTATIVE]	Esterase
16268	2044	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
16272	2045	PHOSPHOFRUCTOKINASE BETA SUBUNIT [PUTATIVE]	Kinase
16280	2046	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
16290	2047	DISEASE RESISTANCE PROTEIN SIMILAR TO RECEPTOR PROTEIN KINASES[PUTATIVE]	Kinase, Protein
16317	2048	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16318	2049	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16319	2050	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16322	2051	RECEPTOR-LIKE PROTEIN KINASE [PUTATIVE]	Kinase, Protein
16325	2052	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
16329	2053	5-ADENYLYLSULFATE REDUCTASE	Reductase
16345	2054	ABC TRANSPORTER SIMILAR TO GUILLARDIA THETA ABC TRANSPORTER, GENBANK ACCESSION NUMBER AF041468[PUTATIVE]	Transporter
16353	2055	POTASSIUM TRANSPORTER SIMILAR TO A. THALIANA K+ ANTIPORTER KEA1, GENBANK ACCESSION NUMBER AF003382[PUTATIVE]	Transporter
16355	2056	PHOSPHATIDYLGLYCEROTRANSFERASE SIMILAR TO CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE OF SYNECHOCYSTIS SP. GENBANK ACCESSION NUMBER D90914[PUTATIVE]	Transferases
16379	2057	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE]	Transporter

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16380	2058	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE]	Transporter
16381	2059	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE]	Transporter
16382	2060	EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1, HOMO SAPIENS, GB:NP_004946[PUTATIVE]	Transporter
16388	2061	RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHAESOLUS VULGARIS, GB:AAD21872	Kinase, Protein
16404	2062	GAG-PROTEASE POLYPROTEIN, GLYCINE MAX., GB: AAC18777[PUTATIVE]	Protease
16406	2063	AAA FAMILY ATPASE BCS1P MITOCHONDRIAL, SACCHAROMYCES CEREVISIAE, SWISS PROT:P32839[PUTATIVE]	ATPase
16407	2064	FERREDOXIN-NADP+ REDUCTASE - LIKE PROTEIN FERREDOXIN-NADP+ REDUCTASE, PISUM SATIVUM, PIR:T06773	Reductase
16411	2065	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR, TRITICUM AESTIVUM, U30323[PUTATIVE]	Glycosylase
16479	2066	REVERSE TRANSCRIPTASE [PUTATIVE]	Transcriptase
16501	2067	GLUCOSYLTRANSFERASE [PUTATIVE]	Transferases
16516	2068	XYLAN ENDOHYDROLASE [PUTATIVE]	Hydrolase
16517	2069	INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE-LIKE PROTEIN INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE (EC 2.7.--)-ARABIDOPSIS THALIANA, PIR2:JC5401	Kinase
16526	2070	PROTEIN PHOSPHATASE 2C - MEDICAGO SATIVA, PID:E305311[PUTATIVE]	Phosphatase
16539	2071	ASCORBATE PEROXIDASE STROMAL	Oxidase
16577	2072	PEROXIDASE C2 PRECURSOR LIKE PROTEIN PEROXIDASE (EC 1.11.1.7) C2 PRECURSOR ARMORACIA RUSTICANA,PID:D1014846	Oxidase
16578	2073	PEROXIDASE C2 PRECURSOR LIKE PROTEIN PEROXIDASE (EC 1.11.1.7) C2 PRECURSOR ARMORACIA RUSTICANA,PID:D1014846	Oxidase

16583	2074	REVERSE TRANSCRIPTASE OF ARABIDOPSIS THALIANA[PUTATIVE]	Transcriptase
16586	2075	ARGINASE SIMILAR TO ARGINASES (PFAM: PF00491, SCORE=353.2, E=1.4E-119, N=1)[PUTATIVE]	AMIDASE
16589	2076	ARGINASE	ARGINASE
16592	2077	PROTEIN DISULFIDE-ISOMERASE [PUTATIVE]	Isomerase
16600	2078	ASCORBATE PEROXIDASE - SPINACIA OLERACEA, PIR2:S66265[PUTATIVE]	Oxidase
16601	2079	ISOAMYLASE-LIKE PROTEIN PROBABLE ISOAMYLASE (EC 3.2.1.68) SU1 - ZEA MAYS, PIR2:T01321	Glycosylase
16608	2080	BETA-1,3-GLUCANASE-LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE TRITICUM AESTIVUM, PIR2:T06268	Glycosylase
16648	2081	ANTHOCYANIN RHAMNOSYLTRANSFERASE -PETUNIA X HYBRIDA, PID:G454253[PUTATIVE]	Transferases
16650	2082	PHOSPHONOPYRUVATE DECARBOXYLASE (EC 4.1.1.-) - METHANOBACTERIUM THERMOAUTOTROPHICUM, PID:G2622714[PUTATIVE]	Decarboxylase
16700	2083	IIBETA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.146) I - MOUSE, PIR1:I56604[PUTATIVE]	Dehydrogenases
16703	2084	LIPASE-LIKE PROTEIN MONOGLYCERIDE LIPASE - MUS MUSCULUS, PID:E1184892	Lipase
16705	2085	DNA-DIRECTED RNA POLYMERASE DNA-DIRECTED RNA POLYMERASE (EC 2.7.7.6) II LARGESTCHAIN - MOUSE, PIR2:A28490[PUTATIVE]	Polymerase
16710	2086	SUCROSE-PHOSPHATE SYNTHASE - LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE, ZEA MAYS, PIR2:JQ1329	Synthase
16724	2087	FRUCTOKINASE - LIKE PROTEIN FRUCTOKINASE, LYCOPERSICON ESCULENTUM, GB:U62329	Kinase
16729	2088	POTASSIUM UPTAKE TRANSPORTER - LIKE PROTEIN POTASSIUM TRANSPORT PROTEIN TRK1, SACCHAROMYCES CEREVISIAE, PIR2:JU0466	Transporter
16737	2089	CLV1 RECEPTOR KINASE, ARABIDOPSIS THALIANA, GB:U96879[PUTATIVE]	Kinase, Protein

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16747	2090	FLAVANONE 3-BETA-HYDROXYLASE NARINGENIN 3-DIOXYGENASE (EC 1.14.11.9) - CHINA ASTER, PIR2:S32147[PUTATIVE]	Oxygenases
16748	2091	FE(II)/ASCORBATE OXIDASE SRG1 PROTEIN ARABIDOPSIS THALIANA, PIR2:S44261[PUTATIVE]	Oxidase
16749	2092	SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM (TOMATO), PID:E1299610[PUTATIVE]	Protease
16750	2093	SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE LYCOPERSICON ESCULENTUM, PID:E1299610[PUTATIVE]	Protease
16751	2094	SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE LYCOPERSICON ESCULENTUM,PID:E1299610[PUTATIVE]	Protease
16752	2095	SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE LYCOPERSICON ESCULENTUM,PID:E1299610[PUTATIVE]	Protease
16753	2096	SUBTILISIN-LIKE PROTEASE -LIKE PROTEIN SUBTILISIN-LIKE PROTEASE AIR3 -ARABIDOPSIS THALIANA,PID:G3695019	Protease
16773	2097	2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ALDOLASES FUNCTIONAL CATALOG ID=01.05[PUTATIVE]	ACID Aldolase
16775	2098	OLIGOPEPTIDE TRANSPORTER SIMILAR TO C. ALBICANS OPT1, GENBANK ACCESSION NUMBER U60973.FUNCTIONAL CATALOG ID=07.99[PUTATIVE]	Transporter
16790	2099	RNA POLYMERASE II TRANSCRIPTION COFACTOR P15, HOMO SAPIENS, PIR2:A54670[PUTATIVE]	Polymerase
16802	2100	PROTEIN PHOSPHOPROTEIN PHOSPHATASE (EC 3.1.3.16) 2C - ARABIDOPSIS THALIANA, PIR2:S55457[PUTATIVE]	Phosphatase
16827	2101	PEROXIDASE ATP19A	Oxidase
16842	2102	MITOCHONDRIAL CARRIER PROTEIN - RIBES NIGRUM,PID:E1313696[PUTATIVE]	Transporter

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16844	2103	SERINE/THREONINE RECEPTOR-LIKE ARABIDOPSIS THALIANA,PID:E1363211	KINASE-LIKE PROTEIN KINASE RLK3	PROTEIN	Kinase, Protein
16845	2104	SERINE/THREONINE RECEPTOR-LIKE ARABIDOPSIS THALIANA,PID:E136321	KINASE-LIKE PROTEIN KINASE RLK3	PROTEIN	Kinase, Protein
16846	2105	SERINE/THREONINE RECEPTOR-LIKE ARABIDOPSIS THALIANA,PID:E136321	KINASE-LIKE PROTEIN KINASE RLK3	PROTEIN	Kinase, Protein
16847	2106	SERINE/THREONINE RECEPTOR-LIKE ARABIDOPSIS THALIANA,PID:E136321	KINASE-LIKE PROTEIN KINASE RLK3	PROTEIN	Kinase, Protein
16848	2107	SERINE/THREONINE (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE RKS1 ARABIDOPSIS THALIANA,PID:G4008008	KINASE-LIKE PROTEIN	PROTEIN	Kinase, Protein
16850	2108	RECEPTOR-LIKE ARABIDOPSIS THALIANA,PID:E136321[PUTATIVE]	PROTEIN KINASE RLK3	-	Kinase, Protein
16851	2109	SERINE/THREONINE (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE RLK3 ARABIDOPSIS THALIANA,PID:E136321	KINASE-LIKE PROTEIN	-	Kinase, Protein
16855	2110	BETA-PHOSPHOGLUCOMUTASE SANFRANCISCO,PID:E1331347[PUTATIVE]	- LACTOBACILLUS	Mutase	
16859	2111	PHOSPHORIBOSYLANTHRANILATE PHOSPHORIBOSYLANTHRANILATE PISUM SATIVUM, D86180[PUTATIVE]	TRANSFERASE TRANSFERASE,	TRANSFERASE	Transferases
16869	2112	REVERSE TRANSCRIPTASE ARABIDOPSIS THALIANA[PUTATIVE]	/TRANSPOSON,	Transposon	Transcriptase
16881	2113	PHOSPHOLIPASE D-GAMMA GAMMA THALIANA,PID:G2653885[PUTATIVE]	PHOSPHOLIPASE D- ARABIDOPSIS	D-	Lipase
16882	2114	PHOSPHOLIPASE D-GAMMA GAMMA THALIANA,PID:G2653885[PUTATIVE]	PHOSPHOLIPASE D- ARABIDOPSIS	D-	Lipase
16883	2115	PHOSPHOLIPASE D-GAMMA GAMMA THALIANA,PID:G2653885[PUTATIVE]	PHOSPHOLIPASE D- ARABIDOPSIS	D-	Lipase

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16887	2116	PROTEIN KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 -ZEA MAYS,PIR2:T02053	Kinase, Protein
16888	2117	KI DOMAIN INTERACTING KINASE 1 -LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 - ZEA MAYS,PID:G2735017	Kinase, Protein
16901	2118	TRANSPORT PROTEIN NA(+) DEPENDENT TRANSPORTER (SBF FAMILY) - AQUIFEX AEOLICUS, PIR2:E70482[PUTATIVE]	Transporter
16923	2119	NUCLEOTIDE SUGAR EPIMERASE -LIKE PROTEIN NUCLEOTIDE SUGAR EPIMERASE -VIBRIO VULNIFICUS,PID:G3093975	Epimerase
16925	2120	COPPER AMINE OXIDASE LIKE PROTEIN (FRAGMENT1) COPPER AMINE OXIDASE - CICER ARIETINUM,PID:E1335964	Oxidase
16926	2121	COPPER AMINE OXIDASE LIKE PROTEIN (FRAGMENT2) COPPER AMINE OXIDASE - CICER ARIETINUM,PID:E1335964	Oxidase
16937	2122	PECTINESTERASE SINENSIS,PID:G2098711[PUTATIVE]	CITRUS Esterase
16941	2123	TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPA) TREHALOSE-6-PHOSPHATE PHOSPHATASE ARABIDOPSIS THALIANA, PID:G2944178[PUTATIVE]	Phosphatase
16980	2124	HYDROLASE-LIKE PROTEIN 2-HYDROXY-6-OXOHEPTA-2,4-DIEOATE HYDROLASE (EC 3.7.-.) SYNECHOCYSTIS SP., PIR2:S77427	Hydrolase
16998	2125	OXIDOREDUCTASE - STREPTOMYCES LIVIDANS,PID:G3293547[PUTATIVE]	Reductase
17002	2126	OLEOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE-LIKE PROTEIN OLEOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE - BRASSICA NAPUS, PIR2:S40407	Hydrolase
17005	2127	ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) - ARABIDOPSIS THALIANA,PIR2:C49539	Transferases
17006	2128	ENDOXYLOGLUCAN TRANSFERASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) - ARABIDOPSIS THALIANA,PIR2:C49539	Transferases

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17015	2129	SHORT-CHAIN ALCOHOL DEHYDROGENASE LIKE PROTEIN SHORT-CHAIN ALCOHOL DEHYDROGENASE - PICEA ABIES, PIR2:S34678	Dehydrogenase
17018	2130	PECTATE LYASE LIKE PROTEIN PECTATE LYASE - FRAGARIA X ANANASSA,PID:G2435395	Lyase
17023	2131	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) (EC1.14.13.8) -ORYCTOLAGUS CUNICULUS,PID:G164989[PUTATIVE]	Oxygenases
17027	2132	TERPENE SYNTHASE TS1, ARABIDOPSIS THALIANA, Y11188[PUTATIVE]	Synthase
17038	2133	CYCLIC BETA-1-3-GLUCAN SYNTHASE, BRADYRHIZOBIUM JAPONICUM, AF047687[PUTATIVE]	Synthase
17039	2134	POTASSIUM TRANSPORTER - LIKE PROTEIN POTASSIUM TRANSPORTER ATKTIP, ARABIDOPSIS THALIANA,AF012656	Transporter
17040	2135	3-ISOPROPYLMALATE DEHYDRATASES/ACONITATE HYDRATASES[PUTATIVE]	Dehydratase
17057	2136	BETA 1,3-GLUCANASE, TRITICUM AESTIVUM, U30323[PUTATIVE]	Glycosylase
17063	2137	ISOFLAVONE REDUCTASE-LIKE PROTEIN ISOFLAVONE REDUCTASE-LIKE PROTEIN, LUPINUS ALBUS, GB:U48590	Reductase
17067	2138	PURPLE ACID PHOSPHATASE IPOMOEA BATATAS, AJ006224[PUTATIVE]	Phosphatase
17068	2139	PECTATE LYASE A11 (FRAGMENT) [PUTATIVE]	Lyase
17073	2140	POLYGALECTURONASE POLYGALECTURONASE, ZEA MAYS, PIR2:S30067[PUTATIVE]	Glycosylase
17106	2141	GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17110	2142	XYLOGLUCAN ENDOTRANSGLYCOSYLASE-RELATED PROTEIN XTR-7	Glycosylase
17118	2143	PHYTOENE DESATURASE, PHYTOENE DEHYDROGENASE PRECURSOR	Desaturases
17140	2144	CARNITINE RACEMASE LIKE PROTEIN	Epimerase
17141	2145	CARNITINE RACEMASE LIKE PROTEIN	Epimerase
17144	2146	REVERSE TRANSCRIPTASE LIKE PROTEIN	Transcriptase

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17154	2147	ACYLAMINOACYL-PEPTIDASE LIKE PROTEIN	Protease
17160	2148	GERMIN PRECURSOR OXALATE OXIDASE	Oxidase
17163	2149	RNA POLYMERASE II FIFTH LARGEST SUBUNIT LIKE PROTEIN	Polymerase
17188	2150	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE	Dehydratase
17218	2151	ABC TRANSPORTER HOMOLOG	Transporter
17222	2152	GLUCOSYLTRANSFERASE	Transferases
17223	2153	UTP-GLUCOSE GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17224	2154	UTP-GLUCOSE GLUCOSYLTRANSFERASE	Transferases
17225	2155	CELLULOSE SYNTHASE LIKE PROTEIN	Synthase
17228	2156	CELLULOSE SYNTHASE LIKE PROTEIN	Synthase
17240	2157	HYDROPEROXIDE LYASE (HPOL) LIKE PROTEIN	Lyase
17244	2158	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17245	2159	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17246	2160	INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17249	2161	PYRUVATE PHOSPHATE DIKINASE PYRUVATE, ORTHOPHOSPHATE DIKINASE	Kinase
17251	2162	GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17261	2163	KINASE LIKE PROTEIN	Kinase, Protein
17283	2164	DELTA-CADINENE SYNTHASE LIKE PROTEIN	Synthase
17294	2165	PECTINESTERASE LIKE PROTEIN	Esterase
17309	2166	GALACTOKINASE LIKE PROTEIN	Kinase
17322	2167	BETA-1,3-GLUCANASE CLASS I PRECURSOR	Glycosylase
17323	2168	PEROXIDASE LIKE PROTEIN	Oxidase
17327	2169	NARINGENIN 3-DIOXYGENASE LIKE PROTEIN	Oxygenases
17353	2170	CELLULOSE SYNTHASE LIKE PROTEIN	Synthase
17354	2171	GLUCOSYLTRANSFERASE LIKE PROTEIN	Transferases
17363	2172	CYANOHYDRIN LYASE LIKE PROTEIN	Lyase
17367	2173	LIMONENE CYCLASE LIKE PROTEIN	Cyclase
17368	2174	LIMONENE CYCLASE LIKE PROTEIN	Cyclase

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17371	2175	GIBBERELLIN OXIDASE-LIKE PROTEIN	Oxidase
17376	2176	TRIACYLGLYCEROL LIPASE LIKE PROTEIN	Lipase
17390	2177	KINASE LIKE PROTEIN	Kinase, Protein
17402	2178	BETA-AMYLASE [PUTATIVE]	Glycosylase
17403	2179	SERINE PROTEASE-LIKE PROTEIN [PUTATIVE]	Protease
17427	2180	PHOSPHORIBOSYLGlyCINAMIDE FORMYLTRANSFERASE-LIKE PROTEIN	Transferases
17464	2181	PEROXIDASE LIKE PROTEIN	Oxidase
17477	2182	N-ACETYLORNITHINE DEACETYLASE-LIKE PROTEIN, FRAGMENT N-ACETYLORNITHINE DEACETYLASE (AODD) - DICTYOSTELIUM DISCOIDEUM, PID:G763048	
17510	2183	POTASSIUM CHANNEL - LIKE PROTEIN KCO1, ARABIDOPSIS THALIANA, Y07825	Channel
17512	2184	POLYGALACTURONASE-LIKE EXOPOLYGALACTURONASE, THALIANA, PIR2:S34266	Glycosylase
17518	2185	STARCH SYNTHASE-LIKE PROTEIN BACTERIAL AND PLANT GLYCOGEN (STARCH) SYNTHASES; FOR EXAMPLE B.SUBTILIS, PATCHX:D1020368	Synthase
17519	2186	RECEPTOR SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR SERINE/THREONINE KINASE PRSK, PATCHX:G1235680	Kinase, Protein
17521	2187	PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE- TRANSFERASE, HAEMOPHILUS INFLUENZAE, PIR2:A64185[PUTATIVE]	Transferases
17523	2188	POTASSIUM CHANNEL PROTEIN KAT2	Channel
17528	2189	BETA-1,3-GLUCANASE-LIKE PROTEIN STRONG SIMLARITY TO ENDO-BETA-1,3-BETA-D- GLUCOSIDASE, NICOTIANA TABACUM, PIR2:S46495	Glycosylase
17538	2190	ADENYLOSUCCINATE LYASE - LIKE PROTEIN ADENYLOSUCCINATE LYASE - HAEMOPHILUS INFLUENZAE	Lyase
17549	2191	LIPASE-LIKE PROTEIN PN47P, IPOMOEA NIL, PID:G1527001	Lipase
17572	2192	CELLULOSE SYNTHASE - LIKE PROTEIN CELLULOSE SYNTHASE, GOSSYPIUM HIRSUTUM, U58283	Synthase

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17576	2193	DNA POLYMERASE III HOLOENZYME TAU SUBUNIT, THERMUS THERMOPHILUS, GB:AF025391[PUTATIVE]	Polymerase
17589	2194	PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE 6, GLYCINE MAX., PIR2:S29851	Kinase, Protein
17593	2195	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE - LIKE PROTEIN XYLOGLUCAN ENDO-TRANSGLYCOSYLASE RELATED PROTEIN XTR-4, ARABIDOPSIS THALIANA, PIR2:S71223	Glycosylase
17596	2196	DNA (CYTOSINE-5-)METHYLTRANSFERASE, ARABIDOPSIS THALIANA, PIR2:S59604[PUTATIVE]	Transferases
17635	2197	PECTINACETYLESTERASE PROTEIN PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR2:S68805[PUTATIVE]	Esterase
17636	2198	PECTINACETYLESTERASE PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR2:S68805[PUTATIVE]	Esterase
17662	2199	FE(II) TRANSPORT PROTEIN FE(II) TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, GB:U27590[PUTATIVE]	Transporter
17663	2200	FE(II) TRANSPORT PROTEIN	Transporter
17665	2201	ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE - LIKE PROTEIN AK-HSDH BIFUNCTIONAL ENZYME PRECURSOR, ARABIDOPSIS THALIANA, PIR2:S46497	Dehydrogenases
17666	2202	CHITINASE / LYSOZYME PZ PRECURSOR, NICOTIANA TABACUM, PIR2:S51591[PUTATIVE]	Chitinase
17668	2203	CHITINASE / LYSOZYME PZ PRECURSOR, NICOTIANA TABACUM, PIR2:S51591[PUTATIVE]	Chitinase
17677	2204	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKB-P TYPE, SYNECHOCYSTIS SP., PIR2:S75144[PUTATIVE]	Isomerase
17688	2205	POTASSIUM TRANSPORTER-LIKE PROTEIN PUTATIVE POTASSIUM TRANSPORTER ATKT2P & ATKT1P, ARABIDOPSIS THALIANA, PATCHX:G2384669 & PATCHX:G2384671	Transporter
17700	2206	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, PARTIAL CDS, PISUM SATIVUM, PATCHX:D1013719	Transferases

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17703	2207	VACUOLAR SORTING RECEPTOR-LIKE PROTEIN BP-80 VACUOLAR SORTING RECEPTOR, PISUM SATIVUM, PATCHX:G1737222	Receptor
17712	2208	TERPENE CYCLASE LIKE PROTEIN 5-EPI- ARISTOLOCHENE SYNTHASE, NICOTIANA TABACUM, PATX:G505588	Cyclase
17713	2209	CADINENE SYNTHASE LIKE PROTEIN (+)-DELTA- CADINENE SYNTHASE ISOZYME XC14, GOSSYPIUMARBOREUM, PIR2:S68366	Synthase
17715	2210	TERPENE CYCLASE LIKE PROTEIN VETISPIRADIENE SYNTHASE, HYOSCYAMUS MUTICUS, PATX:G763421	Cyclase
17719	2211	CLV1 RECEPTOR KINASE LIKE PROTEIN CLAVATA1 RECEPTOR KINASE, ARABIDOPSIS TH., PATX:G2160756	Kinase, Protein
17744	2212	RNA-DIRECTED DNA POLYMERASE, ARABIDOPSIS THALIANA, PIR:S65815[PUTATIVE]	Polymerase
17745	2213	PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE]	Kinase, Protein
17746	2214	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17747	2215	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17748	2216	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17749	2217	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17750	2218	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17751	2219	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17752	2220	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17753	2221	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17754	2222	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein

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17755	2223	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17756	2224	RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17757	2225	PROTEIN (FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE HOMOLOG RK20-1, PHASEOLUS VULGARIS, GB:AF078082[PUTATIVE]	Kinase, Protein
17758	2226	RECEPTOR-LIKE PROTEIN KINASE, RLK3, ARABIDOPSIS THALIANA, AJ011674[PUTATIVE]	Kinase, Protein
17759	2227	PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE]	Kinase, Protein
17761	2228	PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS THALIANA[PUTATIVE]	Kinase, Protein
17762	2229	PROTEIN KINASE LIKE PROTEINS, ARABIDOPSIS[PUTATIVE]	Kinase, Protein
17770	2230	RECEPTOR-LIKE PROTEIN KINASE, RLK3, ARABIDOPSIS THALIANA, AJ011674[PUTATIVE]	Kinase, Protein
17773	2231	RETICULINE OXIDASE - LIKE PROTEIN RETICULINE OXIDASE (EC 1.5.3.9) PRECURSOR, ESCHSCHOLZIA CALIFORNICA, PIR2:A41533	Oxidase
17774	2232	RETICULINE OXIDASE -LIKE PROTEIN RETICULINE OXIDASE, ESCHSCHOLZIA CALIFORNICA, PIR:A41533	Oxidase
17775	2233	RETICULINE OXIDASE - LIKE PROTEIN RETICULINE OXIDASE PRECURSOR, ESCHSCHOLZIA CALIFORNICA, PIR:A41533	Oxidase
17776	2234	TRIPEPTIDYL-PEPTIDASE II, HOMO SAPIENS, PIR:S54376[PUTATIVE]	Protease
17785	2235	RECEPTOR KINASE-LIKE GENE, ORYZA LONGISTAMINATA, GB:U72725[PUTATIVE]	Kinase, Protein
17790	2236	CARBONIC ANHYDRASE -LIKE PROTEIN CARBONIC ANHYDRASE, ARABIDOPSIS THALIANA, GB:U73462	Anhydrase
17791	2237	CARBONIC ANHYDRASE - LIKE PROTEIN DIOSCORIN CLASS A PRECURSOR, DIOSCOREA CAYENENSIS, PIR:S57766	Anhydrase

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17811	2238	GIBBERELLIN 20-OXIDASE - LIKE PROTEIN GIBBERELLIN C-20 OXIDASE, ORYZA SATIVA, PATCHX:G1854637	Oxidase
17813	2239	UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE, E.COLI, PIR2:S13729[PUTATIVE]	Transferases
17814	2240	RECEPTOR KINASE - LIKE PROTEIN SRK3 RECEPTOR KINASE, BRASSICA OLERACEA, PATCHX:G624943	Kinase, Protein
17827	2241	RECEPTOR KINASE - LIKE PROTEIN RECEPTOR-LIKE KINASE SFR2, BRASSICA OLERACEA, PID:E258943	Kinase, Protein
17828	2242	RECEPTOR-LIKE SERINE/THREONINE PROTEIN KINASE ARK3	Kinase, Protein
17829	2243	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE BRLK, BRASSICA OLERACEA, GB:Y12531	Kinase, Protein
17830	2244	SERINE/THREONINE PROTEIN KINASE - LIKE PROTEIN RECEPTOR PROTEIN KINASE (IRK1), IPOMOEA TRIFIDA, GB:U20948	Kinase, Protein
17831	2245	SERINE/THREONINE KINASE - LIKE PROTEIN	Kinase, Protein
17839	2246	NADH DEHYDROGENASE LIKE PROTEIN NADH DEHYDROGENASE (UBIQUINONE) (EC 1.6.5.3)CHAIN NDI1 YEAST, PIR2:S26704 AND OTHER NADH DEHYDROGENASES	Dehydrogenase
17849	2247	BIFUNCTIONAL NUCLEASE, ZINNIA ELEGANS, GB:U90266[PUTATIVE]	Nuclease
17850	2248	BIFUNCTIONAL NUCLEASE D, ZINNIA ELEGANS, GB:U90266[PUTATIVE]	Nuclease
17853	2249	SERINE PROTEASE - LIKE PROTEIN CUCUMISIN, CUCUMIS MELO, A55800	Protease
17854	2250	SUBTILISIN-LIKE PROTEASE SUBTILISIN-LIKE PROTEASE - LYCOPERSICON ESCULENTUM, AJ006378	Protease
17858	2251	PEPTIDE TRANSPORTER - LIKE PROTEIN PEPTIDE TRANSPORTER (PTR1) - HORDEUM VULGARE, AF023472	Transporter
17859	2252	GIBBERELLIN 3 BETA-HYDROXYLASE - LIKE PROTEIN 3B-HYDROXYLASE, SOLANUM LYCOPERSICUM, AB010992	Hydroxylase
17886	2253	PEROXIDASE PRXR1	Oxidase

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17891	2254	PECTINESTERASE LIKE PROTEIN PECTINESTERASE, LYCOPERSICON ESCULENTUM, PATX:E312172	Esterase
17898	2255	PECTATE LYASE LIKE PROTEIN PECTATE LYASE, ZINNIA ELEGANS, PATX:E283787	Lyase
17899	2256	PECTATE LYASE LIKE PROTEIN PECTATE LYASE, ZINNIA ELEGANS, PATX:E283787	Lyase
17903	2257	SERINE/THREONINE PROTEIN KINASE LIKE PROTEIN SERINE/THREONINE PROTEIN KINASE (ARSK1 GENE), ARABIDOPSIS THALIANA, PATCHX:G1066501	Kinase, Protein
17904	2258	RECEPTOR LIKE PROTEIN (FRAGMENT) ES43 PROTEIN, BARLEY, PIR2:S44281	Receptor
17916	2259	ALTERNATIVE OXIDASE, MANGIFERA INDICA PIR2:S45035[PUTATIVE]	Oxidase
17949	2260	TREHALOSE-6-PHOSPHATE PHOSPHATASE - LIKE PROTEIN TREHALOSE-6-PHOSPHATE PHOSPHATASE (ATTPPA), PID:G2944178	Phosphatase
17963	2261	LEUCINE RICH REPEAT RECEPTOR KINASE-LIKE PROTEIN LEUCINE RICH REPEAT RECEPTOR-LIKE KINASE, ORYZA SATIVA, PATCHX:E267533	Kinase, Protein
17974	2262	BILE ACID SODIUM-DEPENDENT TRANSPORTER, HOMO SAPIENS, PIR2:I38655, PREDICTED PROTEIN ILEAL	Transporter
17977	2263	ANTHOCYANIDIN SYNTHASE - LIKE PROTEIN PUTATIVE LEUCANTHOCYANIDIN DIOXYGENASE, ARABIDOPSIS THALIANA, PID:G1575699	Oxygenases
17978	2264	LEUCANTHOCYANIDIN DIOXYGENASE (LDOX) [PUTATIVE]	Oxygenases
18000	2265	GAMMA-GLUTAMYL CYSTEINE SYNTHETASE	Synthase
18003	2266	PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE KINASE - BRASSICA OLERACEA	Kinase, Protein
18004	2267	SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS	Kinase, Protein
18005	2268	SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS	Kinase, Protein
18008	2269	SERINE/THREONINE KINASE -LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein

18009	2270	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18010	2271	SERINE /THREONINE KINASE - LIKE PROTEIN SERINE /THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18011	2272	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18012	2273	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18013	2274	S-RECEPTOR KINASE 8 PRECURSOR, BRASSICA CAMPESTRIS, PIR:JC2481[PUTATIVE]	Kinase, Protein
18014	2275	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18015	2276	PROTEIN KINASE - LIKE PROTEIN RECEPTOR KINASE 1, BRASSICA RAPA	Kinase, Protein
18016	2277	RECEPTOR PROTEIN KINASE, IPOMOEA TRIFIDA[PUTATIVE]	Kinase, Protein
18017	2278	SERINE/THREONINE KINASE SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18018	2279	SERINE /THREONINE KINASE - LIKE PROTEIN SERINE /THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18019	2280	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEAE	Kinase, Protein
18020	2281	SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1 (KIK1), ZEA MAYS	Kinase, Protein
18021	2282	SERINE/THREONINE KINASE - LIKE PROTEIN KI DOMAIN INTERACTING KINASE 1, ZEA MAYS	Kinase, Protein
18022	2283	SERINE/THREONINE KINASE - LIKE PROTEIN SERINE/THREONINE KINASE, BRASSICA OLERACEA	Kinase, Protein
18024	2284	ACC OXIDASE, NICOTIANA GLUTINOSA[PUTATIVE]	Oxidase
18054	2285	POTASSIUM TRANSPORT PROTEIN (TRH1) HIGH- AFFINITY POTASSIUM TRANSPORT PROTEIN KUP1, ARABIDOPSIS THALIANA, EMBL:AC004165[PUTATIVE]	Transporter
18061	2286	V-ATPASE SUBUNIT G (VAG2 GENE)	ATPase
18064	2287	RECEPTOR KINASE RECEPTOR-LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA RKL1, PID:G4008006[PUTATIVE]	Kinase, Protein

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18072	2288	POLYGALACTURONASE POLYGALACTURONASE (EC 3.2.1.15) - AVOCADO, EMBL:X66426[PUTATIVE]	Glycosylase
18089	2289	CELLULOSE SYNTHASE CATALYTIC SUBUNIT - LIKE PROTEIN CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A), ARABIDOPSIS THALIANA, GB:AF027173	Synthase
18090	2290	CELLULOSE SYNTHASE CATALYTIC SUBUNIT, ARABIDOPSIS THALIANA, GB:AF027173[PUTATIVE]	Synthase
18091	2291	CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A), ARABIDOPSIS THALIANA; GB:AF027173[PUTATIVE]	Synthase
18098	2292	2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASE -ESCHERICHIA COLI,PID:G633197[PUTATIVE]	Aldolase
18104	2293	HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE, PSEUDOMONAS STUTZERI, AF039534[PUTATIVE]	Hydrolase
18128	2294	DIHYDROFOLATE REDUCTASE SCHIZOSACCHAROMYCES POMBE,PID:E1320950[PUTATIVE]	Reductase
18155	2295	TRNA ISOPENTENYLTRANSFERASE TRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8), YEAST (SACCHAROMYCES CEREVISIAE), PIR2:S67176[PUTATIVE]	Transferases
18157	2296	ALLIIN LYASE ALLIIN LYASE (EC 4.4.1.4) PRECURSOR (CYSTEINE SULPHOXIDE LYASE), ONION, PIR2:S29301[PUTATIVE]	Lyase
18168	2297	PECTATE LYASE PECTATE LYASE, MUSA ACUMINATA, PATX:E209876[PUTATIVE]	Lyase
18169	2298	DNA POLYMERASE III LIKE PROTEIN DNA POLYMERASE III GAMMA SUBUNIT - AQUIFEX AEOLICUS, PIR2:A70460	Polymerase
18171	2299	ABC-TYPE TRANSPORT PROTEINS[PUTATIVE]	Transporter
18178	2300	ACID PHOSPHATASE (EC 3.1.3.2) PAP, PHASEOLUS VULGARIS, PIR1:S51031[PUTATIVE]	Phosphatase
18189	2301	ALPHA-AMYLASE - LIKE PROTEIN ALPHA-AMYLASE, VIGNA MUNGO, PIR2:S10514	Glycosylase

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18197	2302	MAGNESIUM-PROTOPORPHYRIN METHYLTRANSFERASE - LIKE PROTEIN MAGNESIUM- PROTOPORPHYRIN IX METHYLTRANSFERASE, SYNECHOCYSTIS SP, PIR2:S71781	IX	Transferases
18199	2303	SUPEROXIDE DISMUTASE (EC 1.15.1.1) (FE)(FRAGMENT)		Mutase
18204	2304	ACID PHOSPHATASE - LIKE PROTEIN ACID PHOSPHATASE-1,LYCOPERSICON ESCULENTUM, SWISS-PROT:P27061		Phosphatase
18214	2305	PECTINESTERASE GROUP I CITRUS SINENSIS, PID:G2098705[PUTATIVE]		Esterase
18215	2306	PECTINESTERASE - CITRUS SINENSIS, PID:G2098705[PUTATIVE]		Esterase
18219	2307	SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, PID:G479047		Oxidase
18220	2308	SRG1-LIKE PROTEIN STRONG HOMOLOGY TO SRG1 PROTEIN, A NEW MEMBER OF THE FE(II)/ASCORBATE OXIDASE SUPERFAMILY, PID:G479047		Oxidase
18226	2309	CLPC PROTEASE - SPINACIA OLERACEA,PID:G4105131[PUTATIVE]		Protease
18228	2310	RECEPTOR KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, RLK3 - ARABIDOPSIS THALIANA,PID:E1363211		Kinase, Protein
18231	2311	GIBBERELLIN 20-OXIDASE - ARABIDOPSIS THALIANA		Oxidase
18259	2312	BETA-CAROTENE HYDROXYLASE		Hydroxylase
18261	2313	GLUTAMINE CYCLOTRANSFERASE PRECURSOR - LIKE PROTEIN GLUTAMINE CYCLOTRANSFERASE PRECURSOR, CARICA PAPAYA, AF061240		Transferases
18270	2314	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (XTR-6)		Glycosylase
18271	2315	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA (FRAGMENT), PIR2:S71222[PUTATIVE]		Glycosylase

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18284	2316	V-ATPASE G-SUBUNIT LIKE PROTEIN G SUBUNIT OF VACUOLAR-TYPE H ⁺ -ATPASE (VAG1) - ARABIDOPSIS THALIANA, PID:E1330303	ATPase
18286	2317	PHOSPHATIDYLSERINE DECARBOXYLASE PHOSPHATIDYLSERINE DECARBOXYLASE (EC 4.1.1.65) 2 - YEAST, PIR2:S64484[PUTATIVE]	Decarboxylase
18287	2318	PEROXIDASE PEROXIDASE (EC 1.11.1.7) PRECURSOR, CATIONIC (CLONEPNC2) - PEANUT, PIR2:B38265[PUTATIVE]	Oxidase
18290	2319	PEROXIDASE PEROXIDASE ATP13A - ARABIDOPSIS THALIANA, PID:E264765[PUTATIVE]	Oxidase
18316	2320	PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE, PRUNUS ARMENIACA, U93272	Kinase
18317	2321	STEROID SULFOTRANSFERASE - LIKE PROTEIN STEROID SULFOTRANSFERASE, BRASSICA NAPUS, AF000307	Transferases
18322	2322	SUBTILISIN PROTEASE - LIKE SUBTILISIN-LIKE PROTEASE, ARABIDOPSIS THALIANA, AF055848	Protease
18336	2323	CALCIUM-DEPENDENT PROTEIN KINASE, ORYZA SATIVA, PIR2:S56652[PUTATIVE]	Kinase, Protein
18343	2324	RECEPTOR PROTEIN KINASE - LIKE PROTEIN CF-2.1, SOLANUM PIMPINELLIFOLIUM	Kinase, Protein
18372	2325	BETA-1,3-GLUCANASE PRECURSOR, ORYZA SATIVA, PID:G4097948[PUTATIVE]	Glycosylase
18379	2326	GLUTAMINE AMIDOTRANSFERASE/CYCLASE	Cyclase
18396	2327	TRYPTOPHAN SYNTHASE BETA-SUBUNIT (TSB2)	Synthase
18397	2328	PROTEIN DISULFIDE-ISOMERASE (EC 5.3.4.1) - ASPERGILLUS NIGER, PID:G899149[PUTATIVE]	Isomerase
18414	2329	DIHYDROKAEMPFEROL 4-REDUCTASE, MEDICAGO SATIVA, PIR2:S61416[PUTATIVE]	Reductase
18418	2330	RECEPTOR LIKE KINASE RECEPTOR-LIKE KINASE SFR2, BRASSICA OLERACEA, PID:E258943[PUTATIVE]	Kinase, Protein
18419	2331	RECEPTOR PROTEIN KINASE RECEPTOR PROTEIN KINASE, IPOMOEA TRIFIDA, PID:G836954[PUTATIVE]	Kinase, Protein

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18433	2332	PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR	Reductase
18438	2333	TRNA NUCLEOTIDYLTRANSFERASE METHANOBACTERIUM THERMOAUTOTROPHICUM, PID:G2621768[PUTATIVE]	Transferases
18445	2334	UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE - LIKE PROTEIN UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PETUNIA HYBRIDA	Transferases
18446	2335	UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE - LIKE PROTEIN UDP RHAMNOSE-ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE, PETUNIA X HYBRIDA, PIR2:S36655	Transferases
18449	2336	CARBOHYDRATE KINASE - LIKE PROTEIN PHOSPHOFRUCTOKINASE, BABESIA CANIS, AJ223322	Kinase
18468	2337	PROTEIN PHOSPHATASE HOMOLOG (PPH1)	Phosphatase
18482	2338	PROTEIN KINASE LEPK7, LYCOPERSICON ESCULENTUM, GB:U89684[PUTATIVE]	Kinase, Protein
18495	2339	ATPASE, HAEMATOBLASTIC IRITANS, U12392[PUTATIVE]	ATPase
18497	2340	PECTINESTERASE LIKE PROTEIN PECTINESTERASE, LYCOPERSICON ESCULENTUM, Z94058	Esterase
18500	2341	DIACYLGLYCEROL KINASE ZETA, HOMO SAPIENS, GB:U94905[PUTATIVE]	Kinase
18501	2342	DIACYLGLYCEROL KINASE (FRAGMENT) PUTATIVE DIACYLGLYCEROL KINASE - ARABIDOPSIS THALIANA, PID:G4454484[PUTATIVE]	Kinase
18510	2343	NADH DEHYDROGENASE NADH DEHYDROGENASE (UBIQUINONE) (EC 1.6.5.3) CHAIN NDII - YEAST, PIR2:S26704[PUTATIVE]	Dehydrogenase
18520	2344	(1-4)-BETA-MANNAN ENDOHYDROLASE MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78) TOMATO, PIR2:T04323[PUTATIVE]	Hydrolase
18523	2345	RECEPTOR PROTEIN KINASE LIKE PROTEIN LECTIN RECEPTOR-LIKE SERINE/THREONINE KINASE LECRK1, ARABIDOPSIS THALIANA, PIR2:S68589	Kinase, Protein

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18528	2346	PROTEIN PHOSPHATASE 2C-LIKE PROTEIN PROTEIN PHOSPHATASE 2C-FISSION YEAST, PIR2:S54297	Phosphatase
18537	2347	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR (RLK5)	Kinase, Protein
18544	2348	PROTEIN (FRAGMENT) PROTEIN KINASE XA21, ORYZA SATIVA, PIR1:A57676[PUTATIVE]	Kinase, Protein
18553	2349	RECEPTOR PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR1:S27756	Kinase, Protein
18555	2350	SERINE/THREONINE KINASE-LIKE PROTEIN RECEPTOR-LIKE SERINE/THREONINE KINASE (RKF2), ARABIDOPSIS THALIANA, EMBL:AF024649	Kinase, Protein
18560	2351	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE- FORMING), SUS SCROFA DOMESTICA, PIR1:A33768[PUTATIVE]	Oxygenases
18573	2352	XYLOGLUCAN ENDOTRANSGLYCOSYLASE - LIKE PROTEIN XYLOGLUCAN ENDOTRANSGLYCOSYLASE 1,FAGUS SYLVATICA, PID:E1354157	Glycosylase
18593	2353	SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN SERINE/THREONINE-SPECIFIC KINASE LECRK1 ARABIDOPSIS THALIANA, PIR2:S68589	Kinase, Protein
18597	2354	RNA-DIRECTED DNA POLYMERASE - ARABIDOPSIS THALIANA RETROTRANSPOSON TA11-1, PIR2:S65812[PUTATIVE]	Polymerase
18606	2355	SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE - ARABIDOPSIS THALIANA, PIR2:S71277[PUTATIVE]	Kinase, Protein
18610	2356	PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE- DEPENDENT PHOSPHOFRUCTO-1-KINASE-LIKE PROTEIN PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE - PRUNUS ARMENIACA (APRICOT),PID:G2688822	Kinase
18614	2357	ACID PHOSPHATASE-LIKE PROTEIN ACID PHOSPHATASE-1 (EC 3.1.3.-) - LYCOPERSICON ESCULENTUM,PIR2:T06587	Phosphatase

18615	2358	ACID PHOSPHATASE-LIKE PROTEIN PHOSPHATASE-1 (EC 3.1.3.-) - LYCOPERSICON ESCULENTUM, PIR2:T06587	ACID Phosphatase
18624	2359	BETA-1,3-GLUCANASE-LIKE PROTEIN GLUCANASE (EC 3.2.1.-) 7 - GLYCINE MAX, PIR2:T05960	Glycosylase
18633	2360	SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE LRRPK, PIR2:T08975	Kinase, Protein
18634	2361	PHOSPHOLIPASE A2-LIKE PROTEIN PUTATIVE PHOSPHOLIPASE A2 - ORYZA SATIVA, PID:E1424908	Lipase
18635	2362	PHOSPHOLIPASE A2 - ORYZA SATIVA, PID:E1424908[PUTATIVE]	Lipase
18642	2363	UDP-N-ACETYLGLUCOSAMINE O-ACYLTRANSFERASE - LIKE PROTEIN UDP-N-ACETYLGLUCOSAMINE O- ACYLTRANSFERASE, ALLOCHROMATIUM VINOsum, GB:L76417	Transferases
18645	2364	CYTIDINE DEAMINASE - LIKE PROTEIN CYTIDINE DEAMINASE 6, ARABIDOPSIS THALIANA, AF080676	Deaminase
18646	2365	CYTIDINE DEAMINASE - LIKE PROTEIN CYTIDINE DEAMINASE 6, ARABIDOPSIS THALIANA, AF080676	Deaminase
18648	2366	CYTIDINE DEAMINASE 7	Deaminase
18649	2367	CYTIDINE DEAMINASE 6 (CDA6)	Deaminase
18650	2368	CYTIDINE DEAMINASE 2 (CDA2)	Deaminase
18651	2369	CYTIDINE DEAMINASE 3 (CDA3)	Deaminase
18652	2370	CYTIDINE DEAMINASE 5 (CDA5)	Deaminase
18653	2371	CYTIDINE DEAMINASE 4 (CDA4)	Deaminase
18662	2372	CYTOKININ OXIDASE - LIKE PROTEIN CYTOKININ OXIDASE, ZEA MAYS, GB:Y18377	Oxidase
18672	2373	THREONINE SYNTHASE	Synthase
18677	2374	CHOLINE MONOOXYGENASE - LIKE PROTEIN CHOLINE MONOOXYGENASE PRECURSOR, SPINACIA OLERACEA, GB:U85780	Oxygenases
18687	2375	SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE LRRPK	Kinase, Protein

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18688	2376	DIHYDROPTEROATE SYNTHASE-LIKE PROTEIN PROBABLE DIHYDROPTEROATE SYNTHASE - PISUM SATIVUM, PIR2:T06595	Synthase
18705	2377	PEROXIDASE ATP8A	Oxidase
18715	2378	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE PRECURSOR	Glycosylase
18716	2379	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D- GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA, PIR2:S71222	Glycosylase
18717	2380	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE-LIKE PROTEIN XYLOGLUCAN ENDO-1,4-BETA-D- GLUCANASE (EC 3.2.1.-) XTR-3 - ARABIDOPSIS THALIANA, PIR2:S71222	Glycosylase
18724	2381	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL-LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL - ARABIDOPSIS THALIANA, PID:E1421684	Channel
18732	2382	NUCLEOTIDE SUGAR EPIMERASE-LIKE PROTEIN NUCLEOTIDE SUGAR EPIMERASE - VIBRIO VULNIFICUS, PID:G3093975	Epimerase
18735	2383	CINNAMOYL-COA REDUCTASE - LIKE PROTEIN CINNAMOYL-COA REDUCTASE, SACCHARUM OFFICINARUM, GB:AJ231134	Reductase
18740	2384	RECEPTOR-LIKE KINASE HOMOLOG SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE - DAUCUS CAROTA, PID:G2224911	Kinase, Protein
18741	2385	ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN - ACINETOBACTER SP., PID:D1013698[PUTATIVE])	Oxygenases
18742	2386	ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN - ACINETOBACTER SP., PID:D1013698[PUTATIVE])	Oxygenases
18743	2387	ANILINE DIOXYGENASE (GMP SYNTHASE LIKE PROTEIN) - ACINETOBACTER SP., PID:D1013698[PUTATIVE]	Oxygenases

18744	2388	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL-LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL ARABIDOPSIS THALIANA, PID:E1421684	Channel
18746	2389	2-ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE AEOLICUS, PIR2:E70476[PUTATIVE]	AQUIFEX Transferases
18783	2390	OMEGA-6 FATTY ACID DESATURASE (FAD6) CHLOROPLAST	Desaturases
18798	2391	SERINE/THREONINE-SPECIFIC PROTEIN KINASE - LIKE SERINE/THREONINE-SPECIFIC PROTEIN KINASE PRO25, ARABIDOPSIS THALIANA, PIR2:A46373	Kinase, Protein
18799	2392	WALL-ASSOCIATED KINASE 1, ARABIDOPSIS THALIANA, GB:AJ009696[PUTATIVE]	Kinase, Protein
18802	2393	1,3-BETA-GLUCANASE - LIKE PROTEIN 1,3-BETA-GLUCANASE PRECURSOR, GOSSYPIUM HIRSUTUM, PIR2:S72529	Glycosylase
18808	2394	DNA TOPOISOMERASE LIKE- PROTEIN BACILLUS SUBTILIS DNA TOPOISOMERASE I; PID:G520753	Isomerase
18809	2395	PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR2:S38326	Kinase, Protein
18810	2396	RECEPTOR-LIKE KINASE, PETUNIA INFLATA, PATCHX:G1931655[PUTATIVE]	Kinase, Protein
18812	2397	RECEPTOR KINASE - LIKE PROTEIN RECEPTOR KINASE, PETUNIA INFLATA, PATCHX:G498278	Kinase, Protein
18816	2398	CATION TRANSPORT PROTEIN CHAC, ESCHERICHIA COLI, PIR2:G64868, PREDICTED PROTEIN	Transporter
18846	2399	CELLULOSE SYNTHASE, AGROBACTERIUM TUMEFACIENS, PIR2:I39714[PUTATIVE]	Synthase
18858	2400	Glutamate KAINEATE RECEPTOR, RATTUS NORVEGICUS, PIR2:I53474[PUTATIVE]	Receptor
18863	2401	PEROXIDASE - LIKE PROTEIN PEROXIDASE, SPINACIA OLERACEA, PID:G1781338	Oxidase

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18865	2402	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE LIKE PROTEIN MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE, CUCUMIS SATIVUS, PID:G1805254	Synthase
18878	2403	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, DIAN THUS CARYOPHYLLUS, Z84384[PUTATIVE]	N-Transferases
18887	2404	SERINE/THREONINE PROTEIN KINASE LIKE PROTEIN VARIOUS PREDICTED PROTEIN KINASES, ARABIDOPSIS THALIANA	Kinase, Protein
18912	2405	MIXED-LINEAGE PROTEIN KINASE, HOMO SAPIENS, PIR:A53800[PUTATIVE]	Kinase, Protein
18917	2406	S-RECEPTOR KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE PK10 PRECURSOR, ORYZA SATIVA, PIR2:S50767	Kinase, Protein
18918	2407	L-ASCORBATE PEROXIDASE - LIKE PROTEIN VARIOUS L-ASCORBATE PEROXIDASES	Oxidase
18923	2408	POLYGALACTURONASE (EC 3.2.1.15)PRECURSOR, LYCOPERSICON ESCULENTUM, PIR2:A25534[PUTATIVE]	Glycosylase
18924	2409	EXOPOLYGALACTURONASE, ARABIDOPSIS THALIANA, PIR2:S34200[PUTATIVE]	Glycosylase
18927	2410	CELLULOSE SYNTHASE CATALYTIC SUBUNIT (RSW1)	Synthase
18940	2411	DIMETHYLANILINE MONOOXYGENASE - LIKE PROTEIN DIMETHYLANILINE MONOOXYGENASE (N- OXIDE-FORMING), SUS SCROFA DOMESTICA, PIR:A33768	Oxygenases
18951	2412	POTASSIUM CHANNEL PROTEIN ATKC POTASSIUM CHANNEL - SOLANUM TUBEROSUM, PATX:E264595	Channel
18957	2413	PROTEIN KINASE PROTEIN KINASE TMK1, ARABIDOPSIS THALIANA, PIR1:JQ1674[PUTATIVE]	Kinase, Protein
18970	2414	PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE PYROPHOSPHATE-- FRUCTOSE-6-PHOSPHATE 1-PHOSPHOTRANSFERASE (EC 2.7.1.90) - ENTAMOEBA HISTOLYTICA, PIR2:S68243[PUTATIVE]	1-Transferases

18981	2415	PROTEIN PHOSPHOPROTEIN ARABIDOPSIS THALIANA, PIR2:S55457[PUTATIVE]	Phosphatase
18988	2416	FE(II) TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, GB:U27590[PUTATIVE]	Transporter
18993	2417	PYRUVATE DECARBOXYLASE-I (PDC1)	Decarboxylase
18997	2418	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE, ESCHERICHIA COLI, PIR2:A44292[PUTATIVE]	Synthase
18998	2419	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE, ESCHERICHIA COLI, PIR2:A44292[PUTATIVE]	Synthase
19008	2420	PECTINESTERASE - LIKE PROTEIN PECTINESTERASE, PRUNUS PERSICA, X95991	Esterase
19009	2421	PECTINESTERASE - LIKE PROTEIN PECTIN METHYLESTERASE-LIKE PROTEIN, ZEA MAYS, Y13285	Esterase
19019	2422	GLYCOGENIN GLUCOSYLTRANSFERASE (EC 2.4.1.186) - HUMAN, PID:G1174167[PUTATIVE]	Transferases
19022	2423	DIHYDROKAEMPFEROL 4-REDUCTASE (EC 1.1.1.219) - SYNECHOCYSTIS, PIR2:S75325[PUTATIVE]	Reductase
19028	2424	PEROXIDASE ATP17A -LIKE PROTEIN PEROXIDASE ATP17A -A.THALIANA,PID:E252638	Oxidase
19029	2425	SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE - LIKE PROTEIN SOMATIC EMBRYOGENESIS RECEPTOR- LIKE KINASE -DAUCUS CAROTA,PID:G2224911	Kinase, Protein
19030	2426	POLYGALACTURONASE(EC 3.2.1.15) PRECURSOR - ERWINIA CAROTOVORA,PID:G42330[PUTATIVE]	Glycosylase
19032	2427	ABC-TYPE TRANSPORT PROTEIN SLL1623 - SYNECHOCYSTIS,PIR2:S74812[PUTATIVE]	Transporter
19037	2428	2-DEHYDRO-3-DEOXYPHOSPHOHEPTONATE ALDOLASE	Aldolase
19039	2429	POTASSIUM TRANSPORTER ATKT5P (ATKT5) [PUTATIVE]	Transporter
19044	2430	CARBONATE DEHYDRATASE - LIKE PROTEIN CARBONATE DEHYDRATASE PRECURSOR, SPINACIA OLERACEA,PIR2:S28797	Dehydratase

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19054	2431	AMINOTRANSFERASE (ASPC FAMILY), AQUIFEX AEOLICUS, PIR2:D70479[PUTATIVE]	Transferases
19063	2432	INOSITOL 1,3,4-TRISPHOSPHATE 5/6-KINASE, ARABIDOPSIS THALIANA, PIR2:JC5401[PUTATIVE]	Kinase
19067	2433	BETA-XYLAN ENDOHYDROLASE -LIKE PROTEIN (1,4)-BETA-XYLAN ENDOHYDROLASE ISOENZYME X-II, HORDEUM VULGARE, GB:U59313	Hydrolase
19068	2434	(1,4)-BETA-XYLAN ENDOHYDROLASE, HORDEUM VULGARE, PID:G1718238[PUTATIVE]	Hydrolase
19069	2435	XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE,PID:G1813595[PUTATIVE]	Hydrolase
19070	2436	XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE,PID:G1813595[PUTATIVE]	Hydrolase
19071	2437	(1,4)-BETA-XYLAN ENDOHYDROLASE, ISOENZYME X-I, HORDEUM VULGARE, PID:G1718236[PUTATIVE]	Hydrolase
19072	2438	XYLAN ENDOHYDROLASE ISOENZYME X-I, HORDEUM VULGARE,PID:G1813595[PUTATIVE]	Hydrolase
19073	2439	PEROXIDASE PEROXIDASE ATP12A, ARABIDOPSIS THALIANA, PID:E264763[PUTATIVE]	Oxidase
19077	2440	PROLYL 4-HYDROXYLASE ALPHA(II)-SUBUNIT, MUS MUSCULUS, PIR2:I49135[PUTATIVE]	Hydroxylase
19078	2441	PROTEIN PHOSPHATASE WIP1, HOMO SAPIENS, PID:G2218063[PUTATIVE]	Phosphatase
19099	2442	GLUCOSYLTRANSFERASE -LIKE PROTEIN IMMEDIATE- EARLY SALICYLATE-INDUCED GLUCOSYLTRANSFERASE, NICOTIANA TABACUM, PIR2:T03747	Transferases
19108	2443	RECEPTOR PROTEIN KINASE - LIKE PROTEIN PROTEIN KINASE TMKL1, ARABIDOPSIS THALIANA, PID:E353150	Kinase, Protein
19109	2444	CINNAMYL ALCOHOL DEHYDROGENASE - LIKE PROTEIN CINNAMYL ALCOHOL DEHYDROGENASE, POPULUS DELTOIDES, PATCHX:G288753	Dehydrogenases
19124	2445	MYOSIN HEAVY CHAIN KINASE B, DICTYOSTELIUM DISCOIDEUM, U90946[PUTATIVE]	Kinase, Protein

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19130	2446	SERINE/THREONINE PROTEIN KINASE DAUCUS CAROTA SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE[PUTATIVE]	Kinase, Protein
19136	2447	SERINE/THREONINE PROTEIN KINASE DAUCUS CAROTA SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE, GB:U93048[PUTATIVE]	Kinase, Protein
19137	2448	FATTY ACID ELONGASE 1, KETOACYL-COA SYNTHASE, THALIANA, GB:U29142[PUTATIVE]	Synthase
19140	2449	ISOFLAVONE REDUCTASE - LIKE PROTEIN ISOFLAVONE REDUCTASE HOMOLOG P3, ARABIDOPSIS THALIANA, PIR2:S57613'	Reductase
19157	2450	ARGININE DECARBOXYLASE SPE2	Decarboxylase
19171	2451	CHALCONE SYNTHASE - LIKE PROTEIN CHALCONE SYNTHASE HOMOLOG PRCHS1, PINUS RADIATA, GB:U90341	Synthase
19174	2452	AMIDASE - LIKE PROTEIN AMIDASE, BACILLUS FIRMUS, GB:U64312	Amidase
19178	2453	PHOSPHOLIPASE C, LISTERIA MONOCYTOGENES, PIR:A37204[PUTATIVE]	Lipase
19179	2454	PHOSPHATIDYL INOSITOL-SPECIFIC PHOSPHOLIPASE C, LISTERIA SEELIGERI, GB:X97014[PUTATIVE]	Lipase
19186	2455	L-ASCORBATE PEROXIDASE	Oxidase
19187	2456	BETA-GALACTOSIDASE - LIKE PROTEIN BETA-D- GALACTOSIDASE, MANGIFERA INDICA, PID:G2209358	Glycosylase
19189	2457	PROTEIN KINASE - LIKE LEUCINE RICH REPEAT RECEPTOR-LIKE KINASE, ORYZA SATIVA, PATCHX:E267533	Kinase, Protein
19201	2458	O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE, PINUS TAEDA, GB:U39301	Transferases
19202	2459	O-METHYLTRANSFERASE - LIKE PROTEIN CAFFEIC ACID O-METHYLTRANSFERASE, PINUS TAEDA, GB:U39301	Transferases
19204	2460	AMINO ACID PERMEASE - LIKE PROTEIN LILY mRNA, LILIUM LONGIFLORUM, GB:D21814	Transporter

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19209	2461	PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR2:S28615[PUTATIVE]	Kinase, Protein
19215	2462	LIGAND-GATED ION CHANNEL PROTEIN, ARABIDOPSIS THALIANA (PREDICTED)[PUTATIVE]	Channel
19216	2463	SUGAR TRANSPORTER PROTEIN SUGAR TRANSPORTER, ARABIDOPSIS THALIANA, DB_XREF=PID:G1495273[PUTATIVE]	Transporter
19228	2464	DIHYDROFLAVONOL-4-REDUCTASE, GERBERA X SP., PIR2:S35189[PUTATIVE]	Reductase
19231	2465	THIOREDOXIN REDUCTASE (NADPH) 2	Reductase
19245	2466	PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR2:S28615	Kinase, Protein
19249	2467	SERINE ACETYLTRANSFERASE, SERINE O-ACETYLTRANSFERASE, ARABIDOPSIS THALIANA, PIR2:S71207[PUTATIVE]	Transferases
19252	2468	POLYGALACTURONASE POLYGALACTURONASE 4, LYCOPERSICON ESCULENTUM, PID:G2459815[PUTATIVE]	Glycosylase
19264	2469	PHOSPHOLIPASE D, ARABIDOPSIS THALIANA, GB:U84568[PUTATIVE]	Lipase
19266	2470	PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT, HOMO SAPIENS, GB:U90441[PUTATIVE]	Hydroxylase
19267	2471	PROCOLLAGEN-PROLINE DIOXYGENASE, CAENORHABDITIS ELEGANS, PIR2:A55069[PUTATIVE]	Oxygenases
19282	2472	ASCORBATE PEROXIDASE ASCORBATE PEROXIDASE, GOSSYPIUM HIRSUTUM, GB:U37060[PUTATIVE]	Oxidase
19302	2473	RECEPTOR PROTEIN KINASE CF-2.1 LEUCINE RICH REPEAT PROTEIN, SOLANUM PIMPINELLIFOLIUM, PATX:G1184075[PUTATIVE]	Kinase, Protein
19322	2474	PEROXIDASE LIKE PROTEIN	Oxidase
19356	2475	GLUCOSYLTRANSFERASE-LIKE PROTEIN	Transferases
19360	2476	GERANYLGERANYL PYROPHOSPHATE SYNTHASE	Synthase
19368	2477	UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN	Transferases
19374	2478	MAP3K-LIKE PROTEIN KINASE	Kinase, Protein

19394	2479	HYDROXYNITRILE LYASE LIKE PROTEIN	Lyase
19395	2480	PECTINESTERASE LIKE PROTEIN	Esterase
19404	2481	RECEPTOR KINASE-LIKE PROTEIN	Kinase, Protein
19428	2482	RECEPTOR KINASE-LIKE PROTEIN	Kinase, Protein
19431	2483	BETA-KETOADIPATE ENOL-LACTONE HYDROLASE, ACINETOBACTER SP., L05770[PUTATIVE]	Hydrolase
19438	2484	PEROXIDASE, PRXR2	Oxidase
19440	2485	PECTINESTERASE LIKE PROTEIN	Esterase
19442	2486	HYDROXYNITRILE LYASE LIKE PROTEIN	Lyase
19445	2487	FORMAMIDASE - LIKE PROTEIN FORMAMIDASE, METHYLOPHILUS METHYLOTROPHUS, PIR2:S74213	Amidase
19447	2488	FORMAMIDASE - LIKE PROTEIN FORMAMIDASE, METHYLOPHILUS METHYLOTROPHUS, PIR2:S74213	Amidase
19452	2489	N-ACETYLTRANSFERASE HOOKLESS 1 [PROBABLE]	Transferases
19470	2490	AMINO-ACID N-ACETYLTRANSFERASE, ESCHERICHIA COLI, PIR1:XYECAA[PUTATIVE]	Transferases
19475	2491	PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) - LIKE PROTEIN	Kinase
19478	2492	AMMONIUM TRANSPORTER SAT1, GLYCINE MAX., AF069738[PUTATIVE]	Transporter
19482	2493	HEXOKINASE - LIKE PROTEIN HEXOKINASE, ARABIDOPSIS THALIANA, PIR2:S71205	Kinase
19486	2494	ENDO-XYLOGLUCAN TRANSFERASE - LIKE PROTEIN ENDO-XYLOGLUCAN TRANSFERASE, GOSSYPIUM HIRSUTUM, D88413	Transferases
19490	2495	UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN	Transferases
19507	2496	CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-1	Dehydrogenases
19508	2497	CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-2	Dehydrogenases
19528	2498	CELLULOSE SYNTHASE - POPULUS ALBA X POPULUS TREMULA (CEL1), PID:G3511285[PUTATIVE]	Synthase
19551	2499	PECTINESTERASE PECTINESTERASE - LYCOPERSICON ESCULENTUM, PID:E312172[PUTATIVE]	Esterase

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19554	2500	GERANYLGERANYL PYROPHOSPHATE SYNTHASE- RELATED PROTEIN	Synthase
19560	2501	PROTEIN PHOSPHATASE-2C PROTEIN PHOSPHATASE- 2C (PP2C) - MESEMBRYANTHEMUM CRYSTALLINUM, PID:G3608412[PUTATIVE]	Phosphatase
19562	2502	MONOOXYGENASE 2 (MO2)	Oxygenases
19563	2503	PHOSPHOLIPASE LIKE PROTEIN ARABIDOPSIS THALIANA PEARLI 4 mRNA, PID:G871782	Lipase
19564	2504	PHOSPHOLIPASE LIKE PROTEIN ARABIDOPSIS THALIANA PEARLI 4 mRNA, PID:G871782	Lipase
19565	2505	PHOSPHATIDYLINOSITOL SYNTHASE PHOSPHATIDYLINOSITOL SYNTHASE (PIS1) ARABIDOPSIS THALIANA, PID:E1313354[PUTATIVE]	Synthase
19567	2506	GALACTOSIDASE LIKE PROTEIN SS-1,4- EXOGALACTANASE (BETA-GALACTOSIDASE) LYCOPERSICON ESCULENTUM,PID:E1363850	Glycosylase
19577	2507	PHOSPHOLIPASE C (EC 3.1.4.3) PRECURSOR,PHOSPHATIDYLINOSITOL-SPECIFIC LISTERIA MONOCYTOGENES, PIR2:A37204[PUTATIVE]	Lipase
19590	2508	RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE RLK3, ARABIDOPSIS THALIANA, AJ011674	Kinase, Protein
19618	2509	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, CATHARANTHUS ROSEUS, Z73295[PUTATIVE]	Kinase, Protein
19619	2510	INOSITOL MONOPHOSPHATASE - LIKE PROTEIN MONO-PHOSPHATASE, STREPTOMYCES ANULATUS, X92429	Phosphatase
19628	2511	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (APL3)	Transferases
19630	2512	NAD(P)H OXIDOREDUCTASE, ISOFLAVONE REDUCTASE - LIKE PROTEIN PYRC2, PYRUS COMMUNIS, AF071477	Reductase
19634	2513	RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR PROTEIN KINASE ERECTA, ARABIDOPSIS THALIANA	Kinase, Protein

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19639	2514	CINNAMYL-ALCOHOL DEHYDROGENASE CAD1	Dehydrogenases
19641	2515	CELLULOSE SYNTHASE CATALYTIC SUBUNIT (ATH-A)	Synthase
19643	2516	UBIQUITIN SPECIFIC PROTEASE 66 - GALLUS GALLUS,PID:G3800764[PUTATIVE]	Protease
19652	2517	MITOCHONDRIAL CARRIER - LIKE PROTEIN AGPET8, ASHBYA GOSSYPII, EMBL:AJ006406	Transporter
19660	2518	SHIKIMATE KINASE - LIKE PROTEIN SHIKIMATE KINASE PRECURSOR, LYCOPERSICON ESCULENTUM, GB:S21584	Kinase
19704	2519	2-DEHYDRO-3-DEOXYPHOSPHOHEPTONATE ALDOLASE	Aldolase
19722	2520	PROTEIN - KINASE PROTEIN KINASE TMK1 (EC 2.7.1.-), RECEPTOR TYPE PRECURSOR, ARABIDOPSIS THALIANA, PIR:JQ1674[PUTATIVE]	Kinase, Protein
19737	2521	ANTHRANILATE N-BENZOYLTRANSFERASE - LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE, CLOVE PINK, PIR:T10717	Transferases
19740	2522	LAX1 / AUX1 -LIKE PERMEASE	Transporter
19741	2523	ALPHA-1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE, HOMO SAPIENS, EMBL:AF141315[PUTATIVE]	Transferases
19742	2524	ALPHA AMYLASE [PUTATIVE]	Glycosylase
19743	2525	PHOSPHATASE (CTDP1), HOMO SAPIENS, EMBL:AF154115; HYPOTHETICAL PROTEIN RNA POLYMERASE II CTD	Phosphatase
19748	2526	PYRUVATE DECARBOXYLASE-LIKE PROTEIN PYRUVATE DECARBOXYLASE (EC 4.1.1.1) PDC1 - ARABIDOPSIS THALIANA, PIR:T05315	Decarboxylase
19749	2527	PYRUVATE DECARBOXYLASE-LIKE PROTEIN PYRUVATE DECARBOXYLASE (EC 4.1.1.1) PDC1 - ARABIDOPSIS THALIANA, PIR:T05315	Decarboxylase
19770	2528	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
19771	2529	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein

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19772	2530	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE - ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
19774	2531	GAMMA-INTERFERON INDUCIBLE LYSOSOMAL THIOL REDUCTASE HOMO SAPIENS, EMBL:AF097362[PUTATIVE]	Reductase
19784	2532	TRANSPORTER PROTEIN NA+/H+ ANTIPORTER PROTEINS[PUTATIVE]	Transporter
19785	2533	TRANSPORTER PROTEIN NA+/H+ ANTIPORTER PROTEINS[PUTATIVE]	Transporter
19786	2534	PROTEIN PHOSPHATASE TYPE 2C - SACCHAROMYCES CEREVISIAE, EMBL:U72346[PUTATIVE]	Phosphatase
19808	2535	PROTEIN KINASE - DIFFERENT SPECIES[PUTATIVE]	Kinase, Protein
19809	2536	(1-4)-BETA-MANNAN ENDOHYDROLASE-LIKE PROTEIN MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78) - LYCOPERSICON ESCULENTUM, PIR:T04323	Hydrolase
19811	2537	RECEPTOR PROTEIN KINASES[PUTATIVE]	Kinase, Protein
19823	2538	PROTEIN KINASE WALL-ASSOCIATED KINASE 2 WAK2 - ARABIDOPSIS THALIANA, EMBL:AJ012423[PUTATIVE]	Kinase, Protein
19833	2539	AMINO ACID TRANSPORT PROTEIN - ARABIDOPSIS THALIANA, EMBL:U39783[PUTATIVE]	Transporter
19839	2540	HYDROLASE AT2G32150 - ARABIDOPSIS THALIANA, EMBL:AC006223[PUTATIVE]	Hydrolase
19841	2541	RIBONUCLEASE II-LIKE PROTEIN RIBONUCLEASE II FAMILY PROTEIN, DEINOCOCCUS RADIODURANS, PIR:C75571	Nuclease
19843	2542	ABC TRANSPORTER -LIKE PROTEIN NBD-LIKE PROTEIN POP, ARABIDOPSIS THALIANA, EMBL:AF127664	Transporter
19845	2543	SERINE/THREONINE-SPECIFIC PROTEIN KINASE NAK	Kinase, Protein
19846	2544	UBIQUITIN-PROTEIN LIGASE E3-ALPHA -LIKE PROTEIN UBIQUITIN-PROTEIN LIGASE E3-ALPHA, MOUSE, PIR:T14318	Ligase
19856	2545	PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF079355[PUTATIVE]	Phosphatase

19892	2546	PROTEIN PHOSPHATASE - LIKE PROTEIN PROTEIN PHOSPHATASE 2C HOMOLOG, MESEMBRYANTHEMUM CRYSTALLINUM, EMBL:AF097667	Phosphatase
19896	2547	PROTEIN KINASE - LIKE PROTEIN KINASE APK2A, ARABIDOPSIS THALIANA, EMBL:D88206	Kinase, Protein
19930	2548	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:ATLECGENE	Kinase, Protein
19943	2549	LYSINE DECARBOXYLASE - LIKE PROTEIN LYSINE DECARBOXYLASE, EIKENELLA CORRODENS, EMBL:U89166	Decarboxylase
19979	2550	MONODEHYDROASCORBATE REDUCTASE (NADH) - LIKE PROTEIN MONODEHYDROASCORBATE REDUCTASE (NADH), CUCUMBER, PIR:JU0182	Reductase
19986	2551	S-RECEPTOR KINASE - LIKE PROTEIN S-RECEPTOR KINASE HOMOLOG PRECURSOR, RICE, PIR:S50767	Kinase, Protein
19990	2552	HISTONE DEACETYLASE -LIKE PROTEIN HISTONE DEACETYLASE, HD2-P39, NUCLEOLAR, ZEA MAYS, PIR:T04141	Esterase
19992	2553	BETA-(1-3)-GLUCOSYL BRADYRHIZOBIUM EMBL:AF047687[PUTATIVE]	TRANSFERASE, JAPONICUM, Transfases
19993	2554	3-DEOXY-D-MANNO-OCTULOSONIC TRANSFERASE -LIKE PROTEIN 3-DEOXY-D-MANNO- OCTULOSONIC ACID TRANSFERASE, ESCHERICHIA COLI, PIR:JU0467	ACID Transfases
20014	2555	LIPASE -LIKE PROTEIN LIPASE ARAB-1, ARABIDOPSIS THALIANA, PIR:S68410	Lipase
20028	2556	PHOSPHOGLYCERATE MUTASE - LIKE PROTEIN	Mutase
20034	2557	CARBONATE DEHYDRATASE - LIKE PROTEIN	Dehydratase
20047	2558	PECTATE LYASE-LIKE PROTEIN	Lyase
20053	2559	S-ADENOSYL-L-METHIONINE:SALICYLIC CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN	ACID Transfases
20054	2560	S-ADENOSYL-L-METHIONINE:SALICYLIC CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN	ACID Transfases

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20068	2561	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE - LIKE PROTEIN FABF 3-OXOACYL-[ACYL-CARRIER-PROTEIN]SYNTHASE II, NEISSERIA MENINGITIDIS, EMBL:U73942	Synthase
20069	2562	FATTY ACID ELONGASE - LIKE PROTEIN KCS1 FATTY ACID ELONGASE 3-KETOACYL-COA, SYNTHASE .1, ARABIDOPSIS THALIANA, EMBL:AF053345	Synthase
20075	2563	SULPHITE REDUCTASE	Reductase
20110	2564	NICOTIANAMINE SYNTHASE (DBJ BAA74589.1)	Synthase
20111	2565	PECTINESTERASE	Esterase
20112	2566	PECTINESTERASE	Esterase
20132	2567	CELLULOSE SYNTHASE CATALYTIC SUBUNIT (GB AAC39336.1)	Synthase
20142	2568	CHALCONE ISOMERASE, CHALCONE-FLAVONONE ISOMERASE [PUTATIVE]	Isomerase
20147	2569	MONOOXYGENASE	Oxygenases
20149	2570	PEROXIDASE	Oxidase
20174	2571	PHOSPHORIBOSYLANTHRANILATE ISOMERASE	Isomerase
20175	2572	LEUCOANTHOCYANIDIN DIOXYGENASE-LIKE PROTEIN	Oxygenases
20178	2573	CATIONIC AMINO ACID TRANSPORTER 1[PUTATIVE]	Transporter
20188	2574	ANTHRANILATE SYNTHASE COMPONENT I-1 PRECURSOR (SP P32068)	Synthase
20201	2575	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN	Transferases
20202	2576	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN	Transferases
20203	2577	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN	Transferases
20204	2578	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN	Transferases
20205	2579	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN	Transferases
20231	2580	SUCROSE TRANSPORTER PROTEIN	Transporter
20244	2581	LYSINE DECARBOXYLASE-LIKE PROTEIN	Decarboxylase
20248	2582	DIADENOSINE 5,5'-P1,P4-TETRAPHOSPHATE HYDROLASE-LIKE PROTEIN	Hydrolase
20286	2583	PEROXIDASE (EMB CAA68212.1)	Oxidase

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20287	2584	PEROXIDASE	Oxidase
20288	2585	LECTIN-LIKE PROTEIN KINASE	Kinase, Protein
20289	2586	PROTEIN PHOSPHATASE 2C-LIKE	Phosphatase
20296	2587	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
20299	2588	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN	Transferases
20300	2589	POLYGALACTURONASE INHIBITING PROTEIN 1; PGIP1 (GB AAF69827.1)	Glycosylase
20301	2590	POLYGALACTURONASE INHIBITING PROTEIN	Glycosylase
20307	2591	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
20313	2592	STEROID SULFOTRANSFERASE-LIKE PROTEIN	Transferases
20314	2593	STEROID SULFOTRANSFERASE-LIKE PROTEIN	Transferases
20321	2594	10-DEACETYLBACCATIN III-10-O-ACETYL TRANSFERASE - TAXUS CUSPIDATA, AF193765, EMBL:AF193765[PUTATIVE]	Transferases
20327	2595	PROTEIN KINASE 6 - GLYCINE MAX, PIR:S29851[PUTATIVE]	Kinase, Protein
20328	2596	PROTEIN KINASE XA21 - ORYZA SATIVA, PIR:A57676[PUTATIVE]	Kinase, Protein
20331	2597	RECEPTOR-LIKE PROTEIN KINASE SEVERAL RECEPTOR-LIKE PROTEIN KINASES	Kinase, Protein
20333	2598	GIBBERELLIN 20-OXIDASE	Oxidase
20341	2599	RECEPTOR-LIKE PROTEIN KINASE-LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE - IPOMOEA NIL (JAPANESE MORNING GLORY), PIR:T18536	Kinase, Protein
20349	2600	AMIDASE [PUTATIVE]	AMIDASE
20350	2601	INOSITOL HEXAKISPHTHATE KINASE 2 - HOMO SAPIENS, EMBL:AF177145[PUTATIVE]	Kinase
20354	2602	PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611	Esterase

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20355	2603	PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611	Esterase
20356	2604	PECTIN METHYL-ESTERASE-LIKE PROTEIN PECTIN METHYL-ESTERASE PER - MEDICAGO TRUNCATULA, EMBL:AJ249611..	Esterase
20361	2605	2-OXOGLUTARATE-DEPENDENT DIOXYGENASE - SOLANUM CHACOENSE, EMBL:AF104925[PUTATIVE]	Oxygenases
20375	2606	RECEPTOR-LIKE PROTEIN KINASE[PUTATIVE]	Kinase, Protein
20384	2607	EXONUCLEASE-LIKE PROTEIN	Nuclease
20385	2608	ALPHA GALACTOSYLTRANSFERASE PROTEIN	Transferases
20398	2609	PROANTHRANILATE N-BENZOYLTRANSFERASE -LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE (EC 2.3.1.144), DIANTHUS CARYOPHYLLUS, PIR:T10717	Transferases
20399	2610	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE - LIKE PROTEIN N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE, IPOMOEA BATATAS, EMBL:AB035183	Transferases
20400	2611	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE - LIKE PROTEIN ANTHRANILATE N- BENZOYLTRANSFERASE, DIANTHUS CARYOPHYLLUS, PIR:T10717	Transferases
20416	2612	GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE - LIKE PROTEIN GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE, BORRELIA HERMSII, EMBL:BH40762	Esterase
20459	2613	LIPASE/HYDROLASE GDSL-like -motif	Lipase
20477	2614	FLAVONOL SYNTHASE (FLS) (SP Q96330)	Synthase
20480	2615	AMINO ACID TRANSPORT PROTEIN AAP2	Transporter
20496	2616	DNA-DIRECTED RNA POLYMERASE III CHAIN C53 - SACCHAROMYCES CEREVISIAE, EMBL:X63501[PUTATIVE]	Polymerase
20498	2617	POTASSIUM TRANSPORT PROTEIN-LIKE SEVERAL POTASSIUM TRANSPORT PROTEINS	Transporter

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20501	2618	HYDROLASE ETBD1 - RHODOCOCCUS SP., EMBL:AB004320[PUTATIVE]	Hydrolase
20528	2619	BETA-GLUCOSIDASE - LIKE PROTEIN BETA-GLUCOSIDASE, GLYCINE MAX, AF000378	Glycosylase
20531	2620	BETA-XYLOSIDASE - LIKE PROTEIN BETA-XYLOSIDASE, HYPOCREA JECORINA, EMBL:Z69257	Glycosylase
20534	2621	PECTIN METHYLESTERASE - LIKE PROTEIN PECTIN METHYLESTERASE, MELANDRIUM ALBUM, EMBL:MAPME	Esterase
20545	2622	CELLULOSE SYNTHASE CATALYTIC SUBUNIT	Synthase
20560	2623	RECEPTOR PROTEIN KINASE -LIKE(FRAGMENT) RECEPTOR-LIKE PROTEIN KINASE ERECTA, ARABIDOPSIS THALIANA, EMBL:AC004484	Kinase, Protein
20563	2624	2,2-DIALKYLGLYCINE DECARBOXYLASE, P.CEPACIA, EMBL:PCDGD[PUTATIVE]	Decarboxylase
20568	2625	TREHALOSE-6-PHOSPHATE PHOSPHATASE -LIKE PROTEIN TREHALOSE-6-PHOSPHATE PHOSPHATASE, ARABIDOPSIS THALIANA, EMBL:AF007779	Phosphatase
20574	2626	(3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE -LIKE PROTEIN BETA-HYDROXYACYL-ACP DEHYDRATASE PRECURSOR, TOXOPLASMA GONDII, EMBL:AF067150	Dehydratase
20577	2627	CIS,CIS-MUCONATE TRANSPORT PROTEIN, ACINETOBACTER CALCOACETICUS, SWISSPROT:MUCK_ACICA[PUTATIVE]	Transporter
20587	2628	SERINE/THREONINE KINASE-LIKE PUTATIVE SERINE/THREONINE KINASE - SORGHUM BICOLOR, EMBL:Y14600	Kinase, Protein
20588	2629	ALPHA-HYDROXYNITRILE LYASE-LIKE PROTEIN ALPHA-HYDROXYNITRILE LYASE HNL4 - MANIHOT ESCULENTA, EMBL:AJ223281	Lyase
20591	2630	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE-LIKE PROTEIN HISTIDINOL-PHOSPHATE AMINOTRANSFERASE - NICOTIANA TABACUM, EMBL:Y09204	Transferases

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20606	2631	PROTEIN PHOSPHATASE PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN PTPLB, MUS MUSCULUS, EMBL:AF169286[PUTATIVE]	Phosphatase
20614	2632	BETA-XYLOSIDASE - LIKE PROTEIN BETA- XYLOSIDASE, ASPERGILLUS NIDULANS, EMBL:ANXLND	Glycosylase
20629	2633	HISTIDINE KINASE - LIKE PROTEIN SENSORY TRANSDUCTION HISTIDINE KINASE SLR1759, SYNECHOCYSTIS SP., PIR:S75142	Kinase, Protein
20639	2634	LIGNOSTILBENE-ALPHA,BETA-DIOXYGENASE GENE, SYNECHOCOCCUS PCC7942, EMBL:AF055873[PUTATIVE]	Oxygenases
20644	2635	CHORISMATE MUTASE CM2	Mutase
20659	2636	SER/THR SPECIFIC PROTEIN KINASE-LIKE PROTEIN PROTEIN KINASE I, POPULUS NIGRA, EMBL:AB041503	Kinase, Protein
20668	2637	SUCROSE-PHOSPHATE SYNTHASE -LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE ISOFORM 1, CITRUS UNSHIU, PIR:S72648	Synthase
20678	2638	GLUTAMATE RECEPTOR GLUR3 LIGAND-GATED CHANNEL-LIKE PROTEIN PRECURSOR, ARABIDOPSIS THALIANA, EMBL:AF167355[PUTATIVE]	Channel
20689	2639	FLAVIN-CONTAINING MONOOXYGENASE, STREPTOMYCES COELICOLOR, PIR:T37052[PUTATIVE]	Oxygenases
20690	2640	SALICYLATE HYDROXYLASE, STREPTOMYCES COELICOLOR, PIR:T36193[PUTATIVE]	Hydroxylase
20693	2641	SERINE/THREONINE PROTEIN KINASE; ARABIDOPSIS THALIANA, SWISSPROT:NAK_ARATH[PUTATIVE]	Kinase, Protein
20695	2642	1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE - LIKE PROTEIN 1-D-DEOXYXYLULOSE 5-PHOSPHATE SYNTHASE, LYCOPERSICON ESCULENTUM, EMBL:AF143812	Synthase
20697	2643	SERINE THREONINE TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615[PUTATIVE]	Kinase, Protein
20711	2644	L-GULONO-GAMMA-LACTONE OXIDASE, RATTUS NORVEGICUS, EMBL:RNFLAVIN[PUTATIVE]	Oxidase

20714	2645	OLIGOPEPTIDE TRANSPORTER PROTEIN LEOPT1 OLIGOPEPTIDE TRANSPORTER, LYCOPERSICON ESCULENTUM, EMBL:AF016713[PUTATIVE]	Transporter
20719	2646	MAP KINASE KINASE KINASE 1, MUS MUSCULUS, EMBL:AF117340[PUTATIVE]	Kinase, Protein
20722	2647	LYSOPHOSPHOLIPASE - LIKE PROTEIN LYSOPHOSPHOLIPASE HOMOLOG LPL1, ORYZA SATIVA, EMBL:AF039531	Lipase
20737	2648	POTASSIUM TRANSPORT PROTEIN GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN KEFB, ESCHERICHIA COLI, SWISSPROT:P45522[PUTATIVE]	Transporter
20745	2649	DIAMINOPIMELATE DECARBOXYLASE - LIKE PROTEIN DIAMINOPIMELATE DECARBOXYLASE, ARABIDOPSIS THALIANA, EMBL:ATH249960	Decarboxylase
20748	2650	ESTERASE - LIKE PROTEIN CINI PROTEIN - IMPORTED, BUTYRIVIBRIO FIBRISOLVENS, PIR:T44624[PUTATIVE]	Esterase
20751	2651	SUBTILISIN-LIKE PROTEASE - LIKE PROTEIN SUBTILISIN-LIKE PROTEASE, ARABIDOPSIS THALIANA, EMBL:AF098632	Protease
20752	2652	LYSINE DECARBOXYLASE - LIKE PROTEIN LYSINE DECARBOXYLASE, EIKENELLA CORRODENS, EMBL:U89166	Decarboxylase
20766	2653	NPK1-RELATED PROTEIN KINASE[PUTATIVE]	Kinase, Protein
20770	2654	TRANSMEMBRANE TRANSPORT PROTEIN[PUTATIVE]	Transporter
20789	2655	GLUCOSYLTRANSFERASE -LIKE PROTEIN GLUCOSYLTRANSFERASE ISS5A, SALICYLATE-INDUCED, COMMON TOBACCO, PIR:T03747	Transferases
20797	2656	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE - LIKE PROTEIN ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE, GARDEN PEA, PIR:T06460	Transferases
20800	2657	CALLOSE SYNTHASE CATALYTIC SUBUNIT -LIKE PROTEIN PUTATIVE CALLOSE SYNTHASE CATALYTIC SUBUNIT (CFL1), GOSSYPIUM HIRSUTUM, EMBL:AF085717	Synthase

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20805	2658	5-FORMYLtetrahydrofolate cyclo-ligase-like protein 5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) - HOMO SAPIENS, EMBL:L38928	Ligase
20816	2659	PROTEIN KINASE-LIKE PROTEIN KINASE 1 PNPK1 - POPULUS NIGRA, EMBL:AB041503	Kinase, Protein
20828	2660	ASPARTATE KINASE	Kinase
20829	2661	PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR, ARABIDOPSIS THALIANA, SWISSPROT:RLK5_ARATH	Kinase, Protein
20841	2662	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, SPODOPTERA FRUGIPERDA, EMBL:SF15038[PUTATIVE]	Isomerase
20842	2663	TRANSALDOLASE - LIKE PROTEIN TRANSALDOLASE, SOLANUM TUBEROSUM, EMBL:U95923	Aldolase
20870	2664	POLYAMINE OXIDASE	Oxidase
20871	2665	24-STEROL C-METHYLTRANSFERASE	Transferases
20874	2666	TRANSPORTER-LIKE PROTEIN	Transporter
20875	2667	TRANSPORTER-LIKE PROTEIN	Transporter
20887	2668	ENDOXYLOGLUCAN TRANSFERASE (DBJ BAA81669.1)	Transferases
20893	2669	CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) (TESTA 4 PROTEIN) (SP P13114)	Synthase
20898	2670	ALPHA-MANNOSIDASE	Glycosylase
20906	2671	ASPARTATE KINASE, LYSINE-SENSITIVE (GB AAB63104.1)	Kinase
20910	2672	ABC TRANSPORTER, ATP-BINDING PROTEIN[PUTATIVE]	Transporter
20913	2673	PEROXIDASE ATP20A (EMB CAA67338.1)	Oxidase
20921	2674	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
20922	2675	PROTOPORPHYRINOGEN IX OXIDASE	Oxidase
20926	2676	RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT N-METHYLTRANSFERASE I, SPINACIA OLERACEA CHLOROPLAST, PIR:T08996[PUTATIVE]	Transferases
20927	2677	KINASE - LIKE PROTEIN RING3 PROTEIN, HOMO SAPIENS, EMBL:X96670	Kinase, Protein

20931	2678	PROTEIN ESTERASE HDE, PETROLEUM-DEGRADING BACTERIUM HD-1, EMBL:AB029896[PUTATIVE]	Esterase
20946	2679	TRNA SYNTHASE - LIKE PROTEIN TRNA PSEUDOURIDINE SYNTHASE, FLAVOBACTERIUM JOHNSONIAE, EMBL:AF169967	Synthase
20948	2680	N-ACETYLGLUCOSAMINYLTRANSFERASE III, MUS MUSCULUS, EMBL:MMU66844[PUTATIVE]	Transferases
20957	2681	HIGH AFFINITY NITRATE TRANSPORTER - LIKE PROTEIN HIGH AFFINITY NITRATE TRANSPORTER, ORYZA SATIVA, EMBL:AB008519	Transporter
20962	2682	DNA METHYLTRANSFERASE 3, DANIO RERIO, EMBL:AF135438[PUTATIVE]	Transferases
20965	2683	POLYGALACTURONASE - LIKE PROTEIN POLYGALACTURONASE PG1, GLYCINE MAX, EMBL:AF128266	Glycosylase
20970	2684	CINNAMOYL COA REDUCTASE - LIKE PROTEIN CINNAMOYL COA REDUCTASE, POPULUS TREMULOIDES, EMBL:AF217958	Reductase
20974	2685	CARBONIC ANHYDRASE 2	Anhydrase
20978	2686	FORMATE DEHYDROGENASE (FDH)	Dehydrogenases
20986	2687	GLUCOSYLTRANSFERASE -LIKE PROTEIN GLUCOSYLTRANSFERASE IS5A, COMMON TOBACCO, PIR:T03747	Transferases
20987	2688	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL -LIKE PROTEIN CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL CNGC6, ARABIDOPSIS THALIANA, EMBL:ATH17914	Channel
20988	2689	CATION TRANSPORT PROTEIN PUTATIVE POTASSIUM TRANSPORTER ATKT2P, ARABIDOPSIS THALIANA, EMBL:AF012657[PUTATIVE]	Transporter
20995	2690	ALPHA-MANNOSIDASE -LIKE PROTEIN MANNOSYL OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE, MOUSE, PIR:A41641	Glycosylase
20998	2691	LYSOPHOSPHOLIPASE -LIKE PROTEIN LYSOPHOSPHOLIPASE HOMOLOG (HU-K5), HUMAN, EMBL:HSU67963	Lipase

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21008	2692	SERINE/THREONINE SPECIFIC PROTEIN KINASE -LIKE SERINE/THREONINE/TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615	Kinase, Protein
21009	2693	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN HSR2	Channel
21010	2694	AUXIN TRANSPORT PROTEIN - - - LIKE AUXIN TRANSPORT PROTEIN (PIN7), ARABIDOPSIS THALIANA, EMBL:AF087820	Transporter
21011	2695	PECTATE LYASE -LIKE PROTEIN PECTATE LYASE LAT59, TOMATO, PIR:S27098	Lyase
21018	2696	PRX10 PEROXIDASE - - - LIKE PROTEIN PRX10 PEROXIDASE, SPINACIA OLERACEA, EMBL:SOY16776	Oxidase
21024	2697	AMINO ACID TRANSPORT PROTEIN, ARABIDOPSIS THALIANA, EMBL:U39783[PUTATIVE]	Transporter
21038	2698	DNA METHYLTRANSFERASE 3, DANIO RERIO, EMBL:AF135438[PUTATIVE]	Transferases
21039	2699	RNA METHYLASE - LIKE PROTEIN RNA METHYLASE SPOU, AQUIFEX AEOLICUS, PIR:H70443	Methylase
21041	2700	CYCLIC NUCLEOTIDE-GATED CATION CHANNEL	Channel
21063	2701	PHYTOCHELATIN SYNTHETASE PUTATIVE PHYTOCHELATIN SYNTHETASE - ARABIDOPSIS THALIANA, EMBL:AJ006787[PUTATIVE]	Synthase
21064	2702	MITOCHONDRIAL CARRIER PROTEIN MITOCHONDRIAL CARRIER PROTEIN - RIBES NIGRUM, EMBL:AJ007580[PUTATIVE]	Transporter
21073	2703	SERINE/THREONINE-SPECIFIC PROTEIN KINASE-LIKE PROTEIN SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15 - NICOTIANA TABACUM	Kinase, Protein
21086	2704	CARBOXYLESTERASE-LIKE PROTEIN STEROL ESTERASE - RATTUS NORVEGICUS, EMBL:Z22803	Esterase
21087	2705	BETA-GLUCAN-ELICITOR RECEPTOR - GLYCINE MAX, EMBL:D78510[PUTATIVE]	Receptor
21094	2706	PROTOCHLOROPHYLLIDE REDUCTASE HOMOLOG - ORYZA SATIVA, EMBL:AF093628[PUTATIVE]	Reductase

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21100	2707	RECEPTOR PROTEIN KINASE-LIKE PROTEIN PROBABLE SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE - DAUCUS CAROTA, EMBL:U93048	Kinase, Protein
21101	2708	STEROID S ALPHA-REDUCTASE-LIKE PROTEIN STEROID S ALPHA-REDUCTASE - RATTUS NORVEGICUS, PIR:A34239	Reductase
21112	2709	LIPASE-LIKE PROTEIN MONOGLYCERIDE LIPASE - MUS MUSCULUS, EMBL:AJ001118	Lipase
21119	2710	CELLULOSE SYNTHASE CELA - RHIZOBIUM LEGUMINOSARUM, EMBL:AF121340[PUTATIVE]	Synthase
21123	2711	STEAROYL-ACYL CARRIER PROTEIN DESATURASE STEAROYL-ACYL CARRIER PROTEIN DESATURASE SAD1 - LINUM USITATISSIMUM, EMBL:AJ006957	Desaturases
21124	2712	STEAROYL-ACYL CARRIER PROTEIN DESATURASE STEAROYL-ACYL CARRIER PROTEIN DESATURASE SAD1 - LINUM USITATISSIMUM, EMBL:AJ006957	Desaturases
21129	2713	ACETOLACTATE SYNTHASE-LIKE PROTEIN	Synthase
21139	2714	ACETYL-COA CARBOXYLASE, BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) (SP Q42533)	Carboxylase
21141	2715	N- HYDROXYCINNAMOYL/BENZOYLTRANSFERASE[PUTATIVE]	Transferases
21145	2716	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE-LIKE PROTEIN	Transferases
21148	2717	TYROSINE PHOSPHATASE[PUTATIVE]	Phosphatase
21150	2718	PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
21153	2719	AUXIN TRANSPORT PROTEIN[PUTATIVE]	Transporter
21159	2720	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
21169	2721	CELLULASE (EC 3.2.1.4) PRECURSOR - XANTHOMONAS CAMPESTRIS PV. CAMPESTRIS, PIR:JH0158[PUTATIVE]	Cellulase
21179	2722	N-ACETLYTRANSFERASE F13E7.7 - ARABIDOPSIS THALIANA, EMBL:AC018363[PUTATIVE]	Transferases

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21189	2723	RECEPTOR PROTEIN KINASE -LIKE PROTEIN SERINE/THREONINE-SPECIFIC RECEPTOR PROTEIN KINASE (EC 2.7.1.-), ARABIDOPSIS THALIANA, PIR:S71277	Kinase, Protein
21190	2724	CELLULOSE SYNTHASE CATALYTIC SUBUNIT -LIKE PROTEIN ATH-B, CELLULOSE SYNTHASE CATALYTIC SUBUNIT, ARABIDOPSIS THALIANA, EMBL:AF027174	Synthase
21200	2725	SUGAR TRANSPORTER - LIKE PROTEIN D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER), LACTOBACILLUS BREVIS, SWISSPROT:XYLT_LACBR	Transporter
21202	2726	UDP GLUCOSE:FLAVONOID GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000372	Transferases
21203	2727	UDP GLUCOSE:FLAVONOID GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000371	Transferases
21204	2728	UDP GLUCOSE:FLAVONOID GLUCOSYLTRANSFERASE -LIKE PROTEIN UDP GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE, VITIS VINIFERA, EMBL:AF000372	Transferases
21219	2729	POLYGALACTURONASE-LIKE PROTEIN	Glycosylase
21221	2730	GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN	Transferases
21222	2731	PHYTOENE SYNTHASE (GB AAB65697.1)	Synthase
21232	2732	GLUTAMATE DECARBOXYLASE I (GAD 1) (SP Q42521)	Decarboxylase
21241	2733	CELLULOSE SYNTHASE CATALYTIC SUBUNIT (IRX3)	Synthase
21252	2734	PHOSPHOGLUCOMUTASE-LIKE PROTEIN PHOSPHOGLUCOMUTASE, CHLOROPLAST - SPINACIA OLERACEA, EMBL:X75898	Mutase
21281	2735	PEROXIDASE ATP13A	Oxidase
21291	2736	5-METHYLtetrahydropteroyltriglutamate--HOMOCYSTEINE S-METHYLTRANSFERASE	Transferases
21297	2737	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE-LIKE PROTEIN	Transferases

21298	2738	ANTHРАNILATE PHOSPHORIBOSYLTRANSFERASE, CHLOROPLAST PRECURSOR (SP Q02166)	Transferases
21311	2739	PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN[PUTATIVE]	Isomerase
21319	2740	GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE- LIKE PROTEIN	Transferases
21321	2741	BETA-1,3-GLUCANASE-LIKE PROTEIN	Glycosylase
21346	2742	RECEPTOR KINASE PK3 PRECURSOR, MAIZE, PIR:T02753[PUTATIVE]	Kinase, Protein
21349	2743	SER/THR SPECIFIC PROTEIN KINASE - LIKE PROTEIN VARIOUS PROTEIN KINASE, ARABIDOPSIS THALIANA	Kinase, Protein
21360	2744	PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503	Kinase, Protein
21365	2745	PROTEIN 2'-HYDROXYISOFLAVONE REDUCTASE (EC 1.3.1.45) - NICOTIANA TABACUM, PIR:T02202[PUTATIVE]	Reductase
21366	2746	BETA-AMYLASE-LIKE PROTEIN BETA-AMYLASE PRUNUS ARMENIACA, EMBL:AF139501	Glycosylase
21390	2747	PROTEIN KINASE - LIKE PROTEIN PTO KINASE INTERACTOR 1 (PTII), LYCOPERSICON ESCULENTUM, EMBL:SL28007	Kinase, Protein
21398	2748	PECTIN METHYL ESTERASE -LIKE PROTEIN PECTIN METHYL ESTERASE, SOLANUM TUBEROSUM, EMBL:AF152172	Esterase
21403	2749	TRNA ISOPENTENYLTRANSFERASE -LIKE PROTEIN TRNA ISOPENTENYLTRANSFERASE; SACCHAROMYCES CEREVIAE, PIR:S67176	Transferases
21421	2750	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (APL1/ADG2)	Transferases
21427	2751	PROTEIN PHOSPHATASE, KINASE ASSOCIATED	Phosphatase
21428	2752	PHOSPHOLIPASE - LIKE PROTEIN VARIOUS PREDICTED PHOSPHOLIPASE PROTEINS	Lipase
21436	2753	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE - LIKE PROTEIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A.THALIANA	Isomerase

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21449	2754	PERMEASE FAMILY PROTEIN TC0205, CHLAMYDIA MURIDARUM, PIR:D81729[PUTATIVE]	Transporter
21457	2755	GLYOXAL OXIDASE PRECURSOR, PHANEROCHAETE CHRYSOSPORIUM, PIR:A48296[PUTATIVE]	Oxidase
21463	2756	PEPTIDE TRANSPORT PROTEIN-LIKE PEPTIDE TRANSPORT PROTEIN - HORDEUM VULGARE, EMBL:AF023472	Transporter
21471	2757	GLUTAMINE-TRNA LIGASE - LUPINUS LUTEUS, EMBL:X91787[PUTATIVE, PROTEIN C-TERMINUS OF]	Ligase
21472	2758	PECTIN METHYLESTERASE-LIKE PROTEIN PECTIN METHYL ESTERASE - SOLANUM TUBEROSUM, EMBL:AF152172	Esterase
21487	2759	PEROXIDASE PEROXIDASE, LYCOPERSICON ESCULENTUM, PIR:S32768	Oxidase
21488	2760	PEROXIDASE ATP N	Oxidase
21503	2761	IPP TRANSFERASE - LIKE PROTEIN TRNA DELTA(2)- ISOPENTENYL PYROPHOSPHATE TRANSFERASE (IPP TRANSFERASE), PSEUDOMONAS PUTIDA, EMBL:AF016312	Transferases
21504	2762	RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:M84659	Kinase, Protein
21527	2763	SUCROSE-PHOSPHATE SYNTHASE-LIKE PROTEIN SUCROSE-PHOSPHATE SYNTHASE (EC 2.4.1.14) ISOFORM 1 - CITRUS UNSHIU, EMBL:AB005023	Synthase
21532	2764	BETA-1,3-GLUCANASE BG4	Glycosylase
21533	2765	BETA-1,3-GLUCANASE BG5	Glycosylase
21538	2766	BETA-1,3-GLUCANASE-LIKE PROTEIN BETA-1,3- GLUCANASE BG4 - A. THALIANA, EMBL:X79694	Glycosylase
21539	2767	ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE-LIKE PROTEIN ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE - PRUNUS ARMENIACA, EMBL:U97530	Oxygenases
21540	2768	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE	Synthase
21547	2769	RECEPTOR PROTEIN KINASE - LIKE PROTEIN KINASE XA21, ORYZA SATIVA, PIR:A57676	Kinase, Protein

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21554	2770	ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE - LIKE ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE, PRUNUS ARMENIACA, EMBL:U97530	Oxygenases
21555	2771	BETA-1,3-GLUCANASE - LIKE PROTEIN BETA-1,3-GLUCANASE BG4 AND BG5, A.THALIANA, EMBL:ATCBG45	Glycosylase
21568	2772	RECEPTOR PROTEIN KINASE - LIKE RECEPTOR-LIKE PROTEIN KINASE PRK1, TOMATO, PIR:T07865	Kinase, Protein
21582	2773	SUCROSE-UDP GLUCOSYLTRANSFERASE	Transferases
21585	2774	PECTINESTERASE - LIKE PROTEIN PROBABLE PECTINESTERASE PRECURSOR, GARDEN PEA, PIR:T06374	Esterase
21586	2775	BETA-1,3-GLUCANASE - LIKE PROTEIN PROBABLE BETA-1,3-GLUCANASE, WHEAT, PIR:T06268	Glycosylase
21593	2776	BETA-GLUCOSIDASE - LIKE PROTEIN BETA-GLUCOSIDASE, COMMON NASTURTIUM, PIR:T10521	Glycosylase
21594	2777	BETA-D-GLUCAN EXOHYDROLASE - LIKE PROTEIN BETA-D-GLUCAN EXOHYDROLASE, NICOTIANA TABACUM, EMBL:AB017502	Hydrolase
21597	2778	5-METHYLtetrahydropteroyltriglutamate-HOMOCYSTEINE S-METHYLTRANSFERASE - LIKE PROTEIN 5-METHYLtetrahydropteroyltriglutamate-HOMOCYSTEINE S-METHYLTRANSFERASE, ARABIDOPSIS THALIANA, EMBL:U97200	Transferases
21605	2779	HOMOSERINE DEHYDROGENASE-LIKE PROTEIN THRA BIFUNCTIONAL ENZYME - ESCHERICHIA COLI, PIR:B64720	Dehydrogenases
21634	2780	PEROXIDASE ATP14A HOMOLOG	Oxidase
21635	2781	ACYL COA REDUCTASE-LIKE PROTEIN	Reductase
21656	2782	PREPHENATE DEHYDRATASE/CHORISMATE MUTASE-LIKE PROTEIN	Dehydratase
21658	2783	HISTONE DEACETYLASE-LIKE PROTEIN	Dehydratase
21667	2784	GLUCOSYLTRANSFERASE-LIKE PROTEIN	Transferases
21673	2785	LIPASE/HYDROLASE GD\$L-like -motif	Lipase

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21677	2786	PROTEASE-LIKE PROTEIN	Protease
21682	2787	NA+/H+ ANTIPORTER-LIKE PROTEIN	Transporter
21683	2788	NA+/H+ ANTIPORTER-LIKE PROTEIN	Transporter
21688	2789	SERINE CARBOXYPEPTIDASE[PUTATIVE]	Protease
21693	2790	2-ISOPROPYLMALATE SYNTHASE-LIKE; HOMOCITRATE SYNTHASE-LIKE	Synthase
21694	2791	2-ISOPROPYLMALATE SYNTHASE-LIKE PROTEIN	Synthase
21709	2792	SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
21736	2793	FERREDOXIN-THIOREDOXIN REDUCTASE VARIABLE CHAIN[PUTATIVE]	Reductase
21751	2794	PHOSPHOTRANSFERASE[PUTATIVE]	Transferases
21759	2795	POLYA POLYMERASE[PUTATIVE]	Polymerase
21769	2796	GALACTINOL SYNTHASE	Synthase
21771	2797	AMINO ACID TRANSPORTER	Transporter
21776	2798	PECTINACETYLESTERASE	Esterase
21783	2799	ACYLTRANSFERASE	Transferases
21785	2800	DELTA-(+)-CADINENE SYNTHASE (D-CADINENE SYNTHASE)	Synthase
21790	2801	RECEPTOR-PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
21796	2802	PEROXIDASE-LIKE PROTEIN	Oxidase
21797	2803	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
21798	2804	ENDOCHITINASE ACIDIC (DBJ BAA21861.1)	Chitinase
21799	2805	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
21819	2806	STARCH SYNTHASE SOLUBLE	Synthase
21842	2807	FLAVANONE 3-HYDROXYLASE-LIKE PROTEIN	Hydroxylase
21945	2808	FLAVIN-CONTAINING MONOOXYGENASE, RHESUS MACAQUE, SWISSPROT:FMO2_MACMU[PUTATIVE]	Oxygenases
21966	2809	RECEPTOR-LIKE PROTEIN KINASE - LIKE RECEPTOR- LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR:S27756	Kinase, Protein
21974	2810	PROTEIN PHOSPHATASE - LIKE PROTEIN PHOSPHATASE-2C, MESEMBRYANTHEMUM CRYSTALLINUM, AF075579	Phosphatase

21987	2811	LYSINE DECARBOXYLASE, THALIANA[PUTATIVE]	ARABIDOPSIS	Decarboxylase
22004	2812	UTP-GLUCOSE GLUCOSYLTRANSFERASE - LIKE PROTEIN UTP-GLUCOSE GLUCOSYLTRANSFERASE, CASSAVA, PIR:S41951		Transferases
22010	2813	PYRUVATE WATER DIKINASE, ARCHAEOGLOBUS FULGIDUS, PIR:F69338[PUTATIVE]		Kinase
22013	2814	ISOPENICILLIN N EPIMERASE, STREPTOMYCES CLAVULIGERUS, EMBL:M32324[PUTATIVE]		Epimerase
22020	2815	PECTINACETYLESTERASE PRECURSOR - LIKE PROTEIN PECTINACETYLESTERASE PRECURSOR, VIGNA RADIATA, PIR:S68805		Esterase
22034	2816	PECTINESTERASE 2 PRECURSOR, ARABIDOPSIS THALIANA, PIR:PC4168[PUTATIVE]		Esterase
22035	2817	FERROPORTIN1, MUS MUSCULUS		Transporter
22041	2818	RNA METHYLASES[PUTATIVE]		Methylase
22047	2819	DNA POLYMERASE SUBUNIT [PUTATIVE]		Polymerase
22063	2820	ION CHANNEL - LIKE PROTEIN LIGAND GATED CHANNEL-LIKE PROTEIN, BRASSICA NAPUS, EMBL:AF226613[PUTATIVE]		Channel
22074	2821	G protein SEVEN TRANSMEMBRANE DOMAIN ORPHAN RECEPTOR, MUS MUSCULUS, EMBL:AF051098[PUTATIVE]		Receptor
22094	2822	AMINO ACID AMINOTRANSFERASE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE -- PSEUDOMONAS AERUGINOSA, SWISSPROT:ILVE_PSEAE[PUTATIVE]		Transferases
22096	2823	SIGNAL PEPTIDASE		Protease
22104	2824	PROTEIN KINASE-LIKE PROTEIN MAP3KA MEK KINASE - ARABIDOPSIS THALIANA, EMBL:U58918		Kinase, Protein
22106	2825	POLYGALACTURONASE-LIKE POLYGALACTURONASE - LYCOPERSICON ESCULENTUM, EMBL:AF118567	PROTEIN	Glycosylase
22132	2826	PROTEIN KINASE - LIKE PROTEIN MEKK5 (ASK1, MAPKKK5) GENE FOR MAP/ERK KINASE KINASE 5, HOMO SAPIENS, TREMBL:HS325F22		Kinase, Protein

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22140	2827	PECTIN METHYL-ESTERASE - LIKE PROTEIN PECTIN METHYL-ESTERASE PER, MEDICAGO TRUNCATULA, EMBL:MTR249611	Esterase
22146	2828	PROTEIN PHOSPHATASE - LIKE PROTEIN PHOSPHATASE-2C, CRYSTALLINUM, EMBL:AF075581	Phosphatase
22189	2829	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 1-AMINOCYCLOPROPANE-1- CARBOXYLATE SYNTHASE - ARABIDOPSIS THALIANA, EMBL:U26542, FRAGMENT OF	Synthase
22221	2830	RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE, MADAGASCAR PERIWINKLE, PIR:T10060	Kinase, Protein
22268	2831	GALACTINOL SYNTHASE - LIKE	Synthase
22340	2832	ADENYLYLATE KINASE -LIKE PROTEIN PREDICTED PROTEINS, ARABIDOPSIS THALIANA	Kinase
22388	2833	RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:ATRLPKB	Kinase, Protein
22390	2834	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE PRK1, LYCOPERSICON ESCULENTUM, PIR:T07865[PUTATIVE]	Kinase, Protein
22424	2835	BETA-1,3-GLUCANASE[PUTATIVE]	Glycosylase
22425	2836	HISTIDINE KINASE-LIKE PROTEIN	Kinase, Protein
22446	2837	SERINE/THREONINE PROTEIN KINASE-LIKE	Kinase, Protein
22475	2838	PROTEIN PHOSPHATASE-2C PP2C-LIKE	Phosphatase
22476	2839	ASPARTYL PROTEASE-LIKE	Protease
22477	2840	GSH-DEPENDENT DEHYDROASCORBATE REDUCTASE I-LIKE	Reductase
22502	2841	GLUCAN SYNTHASE GLUCAN SYNTHASES - DIFFERENT SPECIES[PUTATIVE]	Synthase
22521	2842	TRANSPORTER PROTEIN NA+/H+-EXCHANGING PROTEIN NAPA - ENTEROCOCCUS HIRAE, PIR:A42111[PUTATIVE]	Transporter

22532	2843	CAFFEIC ACID O-METHYLTRANSFERASE-LIKE PROTEIN LIGNIN-BISPECIFIC O-METHYLTRANSFERASE - POPULUS TREMULOIDES, EMBL:X62096	Transferases
22533	2844	SUCROSE SYNTHASE-LIKE PROTEIN SUCROSE SYNTHASE - CITRUS UNSHIU, EMBL:AB022091	Synthase
22560	2845	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
22594	2846	PROTEIN KINASE - LIKE PROTEIN PTO KINASE INTERACTOR 1 (PTI1), LYCOPERSICON ESCULENTUM, EMBL:SL28007	Kinase, Protein
22610	2847	GLUCURONOSYL TRANSFERASE-LIKE PROTEIN GLUCURONOSYL TRANSFERASE-LIKE PROTEIN, TOMATO, PIR:S39507	Transferases
22611	2848	QUINONE OXIDOREDUCTASE (EC 1.6.5.5) P1, ARABIDOPSIS THALIANA, PIR:S57611[PUTATIVE]	Reductase
22616	2849	GLUCOSYLMUTASE-LIKE PROTEIN UDP-GLUCOSE GLUCOSYLMUTASE - SORGHUM BICOLOR, EMBL:AF199453	Transferases
22617	2850	SAMT-LIKE PROTEIN S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE (SAMT)- CLARKIA BREWERI, EMBL:AF133053	Transferases
22619	2851	GLUCOSYLMUTASE-LIKE PROTEIN UDP-GLUCOSE GLUCOSYLMUTASE - SORGHUM BICOLOR, EMBL:AF199453	Transferases
22628	2852	ANTHRANILATE N-BENZOYLTRANSFERASE -LIKE PROTEIN ANTHRANILATE N-BENZOYLTRANSFERASE (EC 2.3.1.144), CLOVE PINK, PIR:T10717	Transferases
22636	2853	WALL-ASSOCIATED KINASE 4 (WAK4), ARABIDOPSIS THALIANA, EMBL:ATH9695	Kinase, Protein
22639	2854	RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698	Kinase, Protein
22640	2855	RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698	Kinase, Protein

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22641	2856	RECEPTOR SERINE/THREONINE PROTEIN KINASE - LIKE RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698	-Kinase, Protein
22656	2857	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) (SP P10798)	Carboxylase
22657	2858	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) (SP P10797)	Carboxylase
22658	2859	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) (SP P10796)	Carboxylase
22668	2860	TRYPTOPHAN SYNTHASE BETA CHAIN	Synthase
22671	2861	PROTEIN KINASE[PUTATIVE]	-Kinase, Protein
22697	2862	TRANSPORTER -LIKE PROTEIN N SYSTEM AMINO ACIDS TRANSPORTER NAT-1, MUS MUSCULUS, EMBL:AF159856	Transporter
22717	2863	RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR-PROTEIN KINASE-LIKE PROTEIN, ARABIDOPSIS THALIANA, PIR:T45786	-Kinase, Protein
22718	2864	RECEPTOR PROTEIN KINASE - LIKE PROTEIN RECEPTOR SERINE/THREONINE KINASE PR5K, ARABIDOPSIS THALIANA, EMBL:AT48698	-Kinase, Protein
22720	2865	ACYLTRANSFERASE - LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708	Transferases
22723	2866	ACYLTRANSFERASE -LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708	Transferases
22724	2867	ACYLTRANSFERASE -LIKE PROTEIN ANTHOCYANIN ACYLTRANSFERASE, PERILLA FRUTESCENS, EMBL:AB029340	Transferases
22754	2868	RECEPTOR PROTEIN KINASE -LIKE PROTEIN PROTEIN KINASE XA21, RICE, PIR:A57676	-Kinase, Protein
22773	2869	PEROXIDASE ATP24A	Oxidase

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22798	2870	DEGP PROTEASE-LIKE PROTEIN DEGP PROTEASE PRECURSOR - ARABIDOPSIS THALIANA, EMBL:AF028842	Protease
22806	2871	POLYGALACTURONASE-LIKE PROTEIN POLYGALACTURONASE PRECURSOR - LYCOPERSICON ESCULENTUM, PIR:S57806	Glycosylase
22830	2872	PEROXIDASE ATP26A	Oxidase
22835	2873	PROTEASE SERINE PROTEINASE DO, BACILLUS SUBTILIS, PIR:A69643[PUTATIVE]	Protease
22853	2874	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE SERINE/THREONINE KINASE RKF2, ARABIDOPSIS THALIANA, EMBL:AF024649	Kinase, Protein
22854	2875	RAFFINOSE SYNTHASE -LIKE PROTEIN RAFFINOSE SYNTHASE RFS, CUCUMIS SATIVUS, EMBL:AF073744	Synthase
22893	2876	AMINO ACID PERMEASE	Transporter
22900	2877	UROPHORPHYRIN III METHYLASE (GB AAB92676.1)	Methylase
22914	2878	LIPASE/HYDROLASE GDSL-like -motif	Lipase
22919	2879	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN	Transferases
22931	2880	PURINE PERMEASE-LIKE PROTEIN	Transporter
22933	2881	RECEPTOR KINASE-LIKE PROTEIN	Kinase, Protein
22937	2882	GLUTATHIONE TRANSFERASE-LIKE	Transferases
22939	2883	GLUTATHIONE TRANSFERASE	Transferases
22941	2884	PROTEIN KINASE-LIKE	Kinase, Protein
22962	2885	FOLYL-POLYGLUTAMATE SYNTHASE-LIKE PROTEIN	Synthase
22975	2886	NA+/H+ ANTIPORTER-LIKE PROTEIN	Transporter
22990	2887	CMP-SIALIC ACID TRANSPORTER-LIKE PROTEIN	Transporter
22994	2888	AMINO ACID PERMEASE-LIKE PROTEIN; PROLINE TRANSPORTER-LIKE PROTEIN	Transporter
23001	2889	POLYGALACTURONASE-LIKE PROTEIN	Glycosylase
23003	2890	LIPASE/HYDROLASE GDSL-like -motif	Lipase
23024	2891	BETA-1,3-GLUCANASE-LIKE PROTEIN	Glycosylase
23026	2892	RECEPTOR LECTIN KINASE-LIKE PROTEIN	Kinase, Protein
23031	2893	LIPASE/HYDROLASE GDSL-like -motif	Lipase

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23032	2894	PEROXIDASE (EMB CAA66960.1)	Oxidase
23035	2895	TETRACYCLINE TRANSPORTER PROTEIN[PUTATIVE]	Transporter
23058	2896	SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
23079	2897	ALLENE OXIDE SYNTHASE (EMB CAA73184.1)	Synthase
23086	2898	BETA-1,3-GLUCANASE-LIKE PROTEIN	Glycosylase
23094	2899	DIHYDROFLAVONOL 4-REDUCTASE	Reductase
23097	2900	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN	Transferases
23116	2901	RECEPTOR KINASE-LIKE PROTEIN	Kinase, Protein
23148	2902	INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA34390.1)	Transporter
23149	2903	PHOSPHATE TRANSPORTER (GB AAB17265.1)	Transporter
23150	2904	INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA24281.1)	Transporter
23151	2905	INORGANIC PHOSPHATE TRANSPORTER (DBJ BAA24282.1)	Transporter
23157	2906	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE	Oxidase
23158	2907	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE	Oxidase
23173	2908	N-CARBAMYL-L-AMINO ACID AMIDOHYDROLASE-LIKE PROTEIN	Hydrolase
23174	2909	SUCROSE TRANSPORTER PROTEIN	Transporter
23189	2910	BETA-KETOACYL-COA SYNTHASE	Synthase
23202	2911	DIMETHYLANILINE MONOOXYGENASE-LIKE	Oxygenases
23216	2912	CELLULOSE SYNTHASE CATALYTIC SUBUNIT-LIKE PROTEIN	Synthase
23265	2913	RIBOSE 5-PHOSPHATE ISOMERASE[PUTATIVE]	Isomerase
23276	2914	TERPENE CYCLASE/SYNTHASE	Cyclase
23281	2915	DNA-3-METHYLADENINE GLYCOSYLASE I[PUTATIVE]	Glycosylase
23283	2916	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
23296	2917	POLYGALACTURONASE-LIKE PROTEIN	Glycosylase
23297	2918	POLYGALACTURONASE	Glycosylase
23331	2919	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE-FORMING)-LIKE PROTEIN	Oxygenases
23341	2920	PECTINACETYLESTERASE	Esterase
23343	2921	BETA-AMYLASE-LIKE	Glycosylase

23351	2922	UREA ACTIVE TRANSPORTER-LIKE PROTEIN	Transporter
23377	2923	SUBTILISIN-LIKE PROTEASE	Protease
23378	2924	SUBTILISIN-LIKE PROTEASE	Protease
23379	2925	LIPASE/HYDROLASE GDSL-like -motif	Lipase
23380	2926	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKBP-TYPE [PUTATIVE]	Isomerase
23384	2927	DNA POLYMERASE III, GAMMA SUBUNIT[PUTATIVE]	Polymerase
23390	2928	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
23391	2929	TYROSINE-SPECIFIC PROTEIN PHOSPHATASE-LIKE PROTEIN	Phosphatase
23392	2930	RECEPTOR KINASE-LIKE PROTEIN	Kinase, Protein
23396	2931	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
23403	2932	LIPASE/HYDROLASE GDSL-like -motif	Lipase
23405	2933	MAGNESIUM CHELATASE SUBUNIT OF PROTOCHLOROPHYLLIDE REDUCTASE	Chelatase
23407	2934	LIPASE/HYDROLASE GDSL-like -motif	Lipase
23408	2935	LIPASE/HYDROLASE GDSL-like -motif	Lipase
23420	2936	SERINE/THREONINE PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
23449	2937	POTASSIUM CHANNEL OUTWARD RECTIFYING KCO	Channel
23467	2938	KINASE[PUTATIVE]	Kinase, Protein
23469	2939	PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
23511	2940	PEROXIDASE	Oxidase
23516	2941	S-RIBONUCLEASE BINDING PROTEIN[PUTATIVE]	Nuclease
23518	2942	SERINE/THREONINE KINASE-LIKE	Kinase, Protein
23556	2943	MEMBRANE CHANNEL PROTEIN-LIKE; AQUAPORIN (TONOPLAST INTRNSIC PROTEIN)-LIKE	Channel
23561	2944	PECTIN METHYLESTERASE-LIKE	Esterase
23592	2945	PYROPHOSPHATE-FRUCTOSE-6-PHOSPHATE PHOSPHOTRANSFERASE-LIKE PROTEIN	1-Transferases
23595	2946	ADENYLATE KINASE[PUTATIVE]	Kinase
23617	2947	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE- LIKE PROTEIN	Transferases
23618	2948	XYLOGLUCAN ENDO-1,4-BETA-D-GLUCANASE	Glycosylase

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23621	2949	LACCASE (DIPHENOL OXIDASE)	Oxidase
23622	2950	TERPENE SYNTHASE	Synthase
23625	2951	POLYGALACTURONASE	Glycosylase
23633	2952	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE	Synthase
23649	2953	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
23651	2954	LIGAND-GATED ION CHANNEL PROTEIN-LIKE; GLUTAMATE RECEPTOR-LIKE	Channel
23652	2955	LIGAND-GATED ION CHANNEL PROTEIN-LIKE; GLUTAMATE RECEPTOR-LIKE	Channel
23656	2956	PECTINESTERASE-LIKE; ALSO HIGHLY SIMILAR TO L-ASCORBATE OXIDASE AND POLLEN-SPECIFIC PROTEIN[PUTATIVE]	Oxidase
23685	2957	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
23695	2958	PANTOATE-BETA-ALANINE LIGASE	Ligase
23701	2959	PECTATE LYASE	Lyase
23704	2960	ANTHRANILATE N-BENZOYLTRANSFERASE	Transferases
23718	2961	FATTY ACID ELONGASE; BETA-KETOACYL-COA SYNTHASE-LIKE PROTEIN	Synthase
23729	2962	PECTIN METHYLESTERASE	Esterase
23730	2963	SUCROSE SYNTHASE	Synthase
23738	2964	PHYTOCHELATIN SYNTHETASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO	Synthase
23747	2965	XYLOSIDASE	Glycosylase
23774	2966	AMINO ACID PERMEASE 6 (EMB CAA65051.1)	Transporter
23777	2967	RECEPTOR PROTEIN KINASE	Kinase, Protein
23780	2968	ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE-LIKE	Transferases
23784	2969	FRO2-LIKE PROTEIN; NADPH OXIDASE-LIKE	Oxidase
23785	2970	FRO1-LIKE PROTEIN; NADPH OXIDASE-LIKE	Oxidase
23786	2971	ELICITOR-INDUCIBLE RECEPTOR-LIKE PROTEIN EIR[PUTATIVE]	Receptor
23787	2972	RECEPTOR PROTEIN KINASE-LIKE	Kinase, Protein
23788	2973	RECEPTOR PROTEIN KINASE-LIKE	Kinase, Protein

23789	2974	RECEPTOR PROTEIN KINASE-LIKE	Kinase, Protein
23792	2975	METHIONINE S-METHYLTRANSFERASE (GB AAD49574.1)	Transferases
23844	2976	ABC TRANSPORTER[PUTATIVE]	Transporter
23870	2977	11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE	Dehydrogenases
23871	2978	11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE	Dehydrogenases
23876	2979	PROTEIN TRANSPORT PROTEIN SEC12P-LIKE	Transporter
23880	2980	11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE	Dehydrogenases
23881	2981	11-BETA-HYDROXYSTEROID DEHYDROGENASE-LIKE	Dehydrogenases
23886	2982	UDP-GLUCOSE:PROTEIN TRANSGLUCOSYLASE; REVERSIBLY GLYCOSYLATED POLYPEPTIDE	Glycosylase
23888	2983	OXIDOREDUCTASE[PUTATIVE]	Reductase
23937	2984	ACID PHOSPHATASE	Phosphatase
23942	2985	GIBBERELLIN 20-OXIDASE-LIKE PROTEIN	Oxidase
23946	2986	RECEPTOR PROTEIN KINASE-LIKE	Kinase, Protein
23953	2987	WAX SYNTHASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO	Synthase
23956	2988	AUTOCRINE MOTILITY FACTOR RECEPTOR[PUTATIVE]	Receptor
23957	2989	TREHALOSE-6-PHOSPHATE PHOSPHATASE	Phosphatase
23959	2990	PECTINESTERASE-LIKE; STRONG SIMILARITY TO POLENN-SPECIFIC PROTEIN[PUTATIVE]	Esterase
23960	2991	PECTINESTERASE	Esterase
23961	2992	PECTINESTERASE	Esterase
23967	2993	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
23982	2994	POTASSIUM/PROTON ANTIPORTER-LIKE PROTEIN	Transporter
23985	2995	PEPTIDASE[PUTATIVE]	Protease
23986	2996	SERINE PROTEASE-LIKE PROTEIN	Protease
23987	2997	PROTEIN PHOSPHATASE-2C; PP2C-LIKE PROTEIN	Phosphatase
23988	2998	PROTEIN KINASE[PUTATIVE]	Kinase, Protein
23992	2999	GIBBERELLIN 20-OXIDASE (EMB CAA58294.1)	Oxidase

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23994	3000	FRUCTOKINASE 1	Kinase
24000	3001	PEROXIDASE	Oxidase
24004	3002	MANDELONITRILE LYASE-LIKE PROTEIN	Lyase
24009	3003	MYOSIN HEAVY CHAIN KINASE[PUTATIVE], CONTAINS SIMILARITY TO	Kinase, Protein
24021	3004	DIHYDRODIPICOLINATE REDUCTASE-LIKE PROTEIN	Reductase
24039	3005	HYALURONAN MEDIATED MOTILITY RECEPTOR-LIKE PROTEIN	Receptor
24068	3006	BETA-CAROTENE HYDROXYLASE	Hydroxylase
24091	3007	ORNITHINE CYCLODEAMINASE[PUTATIVE PROTEIN] CONTAINS SIMILARITY TO]	Deaminase
24119	3008	PROTOCHLOROPHYLLIDE REDUCTASE; OXIDOREDUCTASE REQUIRED FOR SHOOT APEX DEVELOPMENT	Reductase
24120	3009	PROTOCHLOROPHYLLIDE REDUCTASE; OXIDOREDUCTASE REQUIRED FOR SHOOT APEX DEVELOPMENT	Reductase
24123	3010	CYCLIC NUCLEOTIDE-REGULATED ION CHANNEL (EMB CAA76178.1)	Channel
24142	3011	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
24147	3012	PECTINESTERASE	Esterase
24168	3013	ALDO/KETO REDUCTASE-LIKE PROTEIN	Reductase
24191	3014	CAFFEIC ACID 3-O-METHYLTRANSFERASE-LIKE PROTEIN	Transferases
24199	3015	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
24202	3016	METHYLTRANSFERASE-LIKE PROTEIN , RIBOSOMAL PROTEIN L11	Transferases
24209	3017	FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE PROTEIN	Transferases
24210	3018	ETHYLENE-FORMING-ENZYME-LIKE DIOXYGENASE	Oxygenases
24211	3019	FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE PROTEIN	Transferases
24216	3020	FLAVONOL 3-O-GLUCOSYLTRANSFERASE-LIKE	Transferases
24224	3021	IAA-AMINO ACID HYDROLASE HOMOLOG ILL3 (GB AAC31939.1)	Hydrolase

24226	3022	O-METHYLTRANSFERASE	Transferases
24229	3023	PROTOCHLOROPHYLLIDE OXIDOREDUCTASE NADPH (GB AAC49043.1)	A Reductase
24235	3024	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL	Channel
24248	3025	RECEPTOR-PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
24260	3026	1,4-BENZOQUINONE REDUCTASE-LIKE; REPRESSOR BINDING PROTEIN-LIKE	TRP Reductase
24269	3027	SERINE/THREONINE-SPECIFIC PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
24291	3028	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR (SPP14671)	Synthase
24306	3029	PYRUVATE DECARBOXYLASE (GB AAB16855.1)	Decarboxylase
24315	3030	LIPASE/HYDROLASE GDSL-like -motif	Lipase
24328	3031	BETA-1,3-GLUCANASE-LIKE PROTEIN	Glycosylase
24335	3032	S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN	Transferases
24342	3033	WAX SYNTHASE-LIKE PROTEIN	Synthase
24343	3034	WAX SYNTHASE-LIKE PROTEIN	Synthase
24344	3035	WAX SYNTHASE[PUTATIVE], PROTEIN CONTAINS SIMILARITY TO	Synthase
24345	3036	WAX SYNTHASE-LIKE PROTEIN	Synthase
24346	3037	WAX SYNTHASE-LIKE PROTEIN	Synthase
24347	3038	WAX SYNTHASE-LIKE PROTEIN	Synthase
24348	3039	WAX SYNTHASE-LIKE PROTEIN	Synthase
24369	3040	PECTIN METHYLESTERASE [PUTATIVE]	Esterase
24373	3041	POTASSIUM CHANNEL OUTWARD RECTIFYING KCO	Channel
24380	3042	BETA-AMYLASE	Glycosylase
24382	3043	PECTATE LYASE	Lyase
24393	3044	SERINE/THREONINE-SPECIFIC KINASE LIKE PROTEIN	Kinase, Protein
24414	3045	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
24418	3046	NICOTIANAMINE SYNTHASE	Synthase

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24436	3047	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE-LIKE	Transferases
24440	3048	S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL MethylTRANSFERASE-LIKE PROTEIN	Transferases
24443	3049	CARBONIC ANHYDRASE[PUTATIVE, PROTEIN CONTAINS SIMILARITY TO]	Anhydrolase
24469	3050	BETA-1,3-GLUCANASE-LIKE PROTEIN	Glycosylase
24473	3051	PHOSPHOFRUCTO-1-KINASE, PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE-LIKE PROTEIN	Kinase
24475	3052	IAA-AMINO ACID HYDROLASE HOMOLOG I PRECURSOR (SP P54969)	Hydrolase
24476	3053	IAA-AMINO ACID HYDROLASE (GB AAC04866.1)	Hydrolase
24483	3054	ZINC PROTEASE PQQL-LIKE PROTEIN	Protease
24484	3055	HISTONE ACETYLTRANSFERASE HAT B	Transferases
24486	3056	SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52 (PIR S71207)	Transferases
24489	3057	PROTEIN KINASE[PUTATIVE]	Kinase, Protein
24506	3058	CYTOKININ OXIDASE	Oxidase
24512	3059	LYCOPENE EPSILON CYCLASE	Cyclase
24518	3060	AUXIN TRANSPORT PROTEIN EIR1 (GB AAC39513.1)	Transporter
24528	3061	PHOSPHATIDYLSERINE DECARBOXYLASE	Decarboxylase
24555	3062	AAA-TYPE ATPASE[PUTATIVE]	ATPase
24560	3063	XYLOGLUCAN ENDOTRANSGLYCOSYLASE	Glycosylase
24561	3064	XYLOGLUCAN ENDOTRANSGLYCOSYLASE	Glycosylase
24562	3065	ENDOXYLOGLUCAN TRANSFERASE (GB AAD45127.1)	Transferases
24566	3066	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE-LIKE PROTEIN	Transferases
24591	3067	N-HYDROXYCINNAMOYL/BENZOYLTRANSFERASE	Transferases
24592	3068	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE-LIKE PROTEIN	Transferases
24596	3069	ANTHRANILATE SYNTHASE BETA CHAIN	Synthase

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24601	3070	CYCLIC NUCLEOTIDE AND CALMODULIN-REGULATED ION CHANNEL (EMB CAB40130.1)	Channel
24604	3071	DNA-3-METHYLADENINE GLYCOSYLASE [PUTATIVE]	Glycosylase
24616	3072	BETA-1,3 GLUCANASE - LIKE PROTEIN BETA-1,3 GLUCANASE, POPULUS ALBA X POPULUS TREMULA, EMBL:AF230109	Glycosylase
24622	3073	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
24627	3074	PHOSPHOESTERASE [CONTAINS SIMILARITY TO]	Esterase
24637	3075	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
24638	3076	ALPHA-HYDROXYNITRILE LYASE, POLYNEURIDINE ALDEHYDE ESTERASE-LIKE; ALSO SIMILAR TO ALPHA-HYDROXYNITRILE LYASE	Lyase
24646	3077	PEROXIDASE	Oxidase
24647	3078	PEROXIDASE	Oxidase
24655	3079	BETA 1-3 GLUCANASE - LIKE PROTEIN BETA 1-3 GLUCANASE, VITIS VINIFERA, EMBL:VVI277900	Glycosylase
24656	3080	CINNAMOYL-COA REDUCTASE - LIKE PROTEIN CINNAMOYL-COA REDUCTASE, CIDER TREE, PIR:T10733	Reductase
24659	3081	PROTEIN KINASE - LIKE PROTEIN KINASE ATN1, ARABIDOPSIS THALIANA, PIR:S61766	Kinase, Protein
24661	3082	SERINE/THREONINE-SPECIFIC PROTEIN KINASE NPK15, NICOTIANA TABACUM, PIR:S52578[PUTATIVE]	Kinase, Protein
24680	3083	CARBOHYDRATE KINASE, PFKB, ARCHAEOGLOBUS FULgidus, PIR:A69300[PUTATIVE]	Kinase
24701	3084	RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060	Kinase, Protein
24708	3085	PROTEIN KINASE - LIKE SERINE/THREONINE/TYROSINE-SPECIFIC PROTEIN KINASE APK1, ARABIDOPSIS THALIANA, PIR:S28615	Kinase, Protein
24710	3086	COPPER TRANSPORT PROTEIN	Transporter
24711	3087	COPPER TRANSPORT PROTEIN - LIKE	Transporter
24714	3088	HEXOSYLTRANSFERASE - LIKE PROTEIN	Transferases

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24733	3089	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47481	Kinase, Protein
24734	3090	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47481	Kinase, Protein
24759	3091	ZINC TRANSPORTER ZIP2 - LIKE Z25114[PUTATIVE]	Transporter
24760	3092	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE - LIKE PROTEIN 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE KIDNEY BEAN, PIR:T10818	Oxidase
24761	3093	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE - LIKE PROTEIN 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE KIDNEY BEAN, PIR:T10818	Oxidase
24765	3094	GLUCURONOSYL TRANSFERASE - GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED, LYCOPERSICON ESCULENTUM, PIR:S39507	Transferases
24766	3095	GLUCURONOSYL TRANSFERASE - GLUCURONOSYL TRANSFERASE HOMOLOG, RIPENING-RELATED, LYCOPERSICON ESCULENTUM, PIR:S39507	Transferases
24771	3096	SERINE/THREONINE-SPECIFIC PROTEIN KINASE - PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
24772	3097	SERINE/THREONINE-SPECIFIC PROTEIN KINASE - PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
24773	3098	SERINE/THREONINE-SPECIFIC PROTEIN KINASE - PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
24774	3099	SERINE/THREONINE-SPECIFIC PROTEIN KINASE - PUTATIVE PROTEIN SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
24777	3100	RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060	Kinase, Protein

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24781	3101	SERINE /THREONINE KINASE - LIKE PUTATIVE SERINE /THREONINE KINASE, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
24782	3102	GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE - LIKE PROTEIN GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE, ARABIDOPSIS THALIANA, EMBL:ATAJ0053	Synthase
24784	3103	TYROSINE PHOSPHATASE-LIKE PROTEIN, PTPLB, MUS MUSCULUS, EMBL:AF169286[PUTATIVE]	Phosphatase
24788	3104	SUBTILISIN-LIKE PROTEASE - LIKE PROTEIN SUBTILISIN-LIKE PROTEASE AIR3, ARABIDOPSIS THALIANA, EMBL:AF098632	Protease
24815	3105	PROTEIN KINASE - LIKE PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503	Kinase, Protein
24816	3106	PROTEIN KINASE - LIKE PROTEIN KINASE 1, POPULUS NIGRA, EMBL:AB041503	Kinase, Protein
24830	3107	TRNA INTRON ENDONUCLEASE - LIKE PROTEIN TRNA INTRON ENDONUCLEASE, ARABIDOPSIS THALIANA, EMBL:AB036339	Nuclease
24834	3108	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47484	Kinase, Protein
24835	3109	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47484	Kinase, Protein
24837	3110	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:AL138657	Kinase, Protein
24838	3111	RECEPTOR LIKE PROTEIN KINASE RECEPTOR LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, EMBL:AL138657	Kinase, Protein
24839	3112	RECEPTOR-LIKE PROTEIN KINASE RECEPTOR-LIKE PROTEIN KINASE, ARABIDOPSIS THALIANA, PIR:T47473	Kinase, Protein

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24861	3113	IMIDAZOLEGLYCEROL-PHOSPHATE SUBUNIT H - LIKE IMIDAZOLEGLYCEROL-PHOSPHATE SYNTHASE SUBUNIT H HOMOLOG, ARCHAEOGLOBUS FULGIDUS, PIR:E69313	SYNTHASE	Synthase
24884	3114	HIGH-AFFINITY NITRATE TRANSPORTER ACH1 - LIKE PROTEIN HIGH-AFFINITY NITRATE TRANSPORTER ACH1, ARABIDOPSIS THALIANA, EMBL:AF019748	AFFINITY NITRATE TRANSPORTER	Transporter
24885	3115	HIGH AFFINITY NITRATE TRANSPORTER PROTEIN - LIKE PROBABLE HIGH AFFINITY NITRATE TRANSPORTER PROTEIN, GLYCINE MAX, PIR:T06237	NITRATE TRANSPORTER	Transporter
24897	3116	S-RECEPTOR KINASE HOMOLOG 2 PRECURSOR S-RECEPTOR KINASE HOMOLOG 2 PRECURSOR, ARABIDOPSIS THALIANA, PIR:S27754	S-RECEPTOR KINASE HOMOLOG 2 PRECURSOR	Kinase, Protein
24899	3117	PHYTOCHELATIN SYNTHETASE - LIKE PROTEIN PUTATIVE PHYTOCHELATIN SYNTHETASE, ARABIDOPSIS THALIANA, EMBL:ATH6787	PHYTOCHELATIN SYNTHETASE	Synthase
24902	3118	PHYTOCHELATIN SYNTHETASE - LIKE PUTATIVE PHYTOCHELATIN SYNTHETASE, ARABIDOPSIS THALIANA, EMBL:ATH6787[PUTATIVE]	PHYTOCHELATIN SYNTHETASE	Synthase
24923	3119	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE - LIKE PROTEIN ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE, GENTIANA TRIFLORA, EMBL:AB010708	ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE	Transferases
24942	3120	RECEPTOR-LIKE PROTEIN KINASE PRECURSOR - LIKE RECEPTOR-LIKE PROTEIN KINASE PRECURSOR, MADAGASCAR PERIWINKLE, PIR:T10060	RECEPTOR-LIKE PROTEIN KINASE PRECURSOR	Kinase, Protein
24955	3121	LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE - LIKE PROTEIN LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE LRPKMI, MALUS DOMESTICA, EMBL:AF053127	LEUCINE-RICH RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
24964	3122	PROTEIN KINASE-LIKE TRANSMEMBRANE PROTEIN TMKL1 PRECURSOR, ARABIDOPSIS THALIANA, EMBL:ATTMKL1[PUTATIVE]	PROTEIN KINASE-LIKE TRANSMEMBRANE PROTEIN	Kinase, Protein

24965	3123	PHOSPHOFRUCTO-1-KINASE, DEPENDENT PHOSPHOFRUCTO-1-KINASE - LIKE PROTEIN PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTO-1-KINASE, PRUNUS ARMENIACA, EMBL:U93272	Kinase
24975	3124	PECTIN METHYL-ESTERASE - LIKE PROTEIN PECTIN METHYL ESTERASE PEST2, SOLANUM TUBEROSUM, EMBL:AF152172	Esterase
25021	3125	IRON-REGULATED TRANSPORTER - LIKE PROTEIN IRON-REGULATED TRANSPORTER 1, LYCOPERSICON ESCULENTUM, EMBL:AF136579	Transporter
25028	3126	RECEPTOR-LIKE PROTEIN KINASE 5, ARABIDOPSIS THALIANA, PIR:S27756[PUTATIVE]	Kinase, Protein
25053	3127	GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN	Transferases
25058	3128	DEHYDROGENASE	Dehydrogenases
25065	3129	TRANSPORTIN-SR[PUTATIVE]	Transporter
25073	3130	PEPTIDE TRANSPORTER	Transporter
25076	3131	RECEPTOR - LIKE PROTEIN KINASE - LIKE PROTEIN SERINE/THREONINE KINASE RLK1, SORGHUM BICOLOR, EMBL:SBRLK1	Kinase, Protein
25078	3132	NITRATE TRANSPORTER NTL1 - LIKE PROTEIN NITRATE TRANSPORTER NTL1, ARABIDOPSIS THALIANA, EMBL:AF073361	Transporter
25084	3133	1-DEOXY-D-XYLULOSE REDUCTOISOMERASE (DXR)-	Isomerase
25102	3134	DIHYDRONEOPTERIN ALDOLASE-LIKE PROTEIN	Aldolase
25121	3135	LIPASE/HYDROLASE-LIKE PROTEIN	Lipase
25122	3136	PECTATE LYASE	Lyase
25127	3137	BETA-1,3-GLUCANASE-LIKE PROTEIN[PUTATIVE]	Glycosylase
25137	3138	KINASE[PUTATIVE]	Kinase, Protein
25145	3139	RECEPTOR-LIKE PROTEIN KINASE[PUTATIVE]	Kinase, Protein
25155	3140	ACETYLTRANSFERASE[PUTATIVE]	Transferases
25160	3141	ACYLTRANSFERASE-LIKE PROTEIN	Transferases

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25161	3142	GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) (SP P42799)	Transfases
25162	3143	FLAVONOL SYNTHASE	Synthase
25163	3144	FLAVONOL SYNTHASE	Synthase
25164	3145	1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE-LIKE PROTEIN	Oxidase
25175	3146	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
25185	3147	BETA-GALACTOSIDASE (EMB CAB64746.1)	Glycosylase
25189	3148	AMINO ACID TRANSPORTER AAP4 (PIR S51169)	Transporter
25193	3149	HISTIDINOL DEHYDROGENASE	Dehydrogenases
25197	3150	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
25198	3151	PROTEIN KINASE[PUTATIVE]	Kinase, Protein
25214	3152	PEROXIDASE ATP3A (EMB CAA67340.1)	Oxidase
25215	3153	PEROXIDASE ATP3A HOMOLOG	Oxidase
25216	3154	PEROXIDASE (EMB CAA67551.1)	Oxidase
25225	3155	ALTERNATIVE OXIDASE 2 (SP O22049)	Oxidase
25229	3156	2-NITROPROPANE DIOXYGENASE-LIKE PROTEIN	Oxygenases
25234	3157	GTP CYCLOHYDROLASE II; 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE (EMB CAA03884.1)	Synthase
25261	3158	BETA-XYLOSIDASE	Glycosylase
25268	3159	PECTIN METHYLESTERASE-LIKE PROTEIN	Esterase
25278	3160	CELLULOSE SYNTHASE CATALYTIC SUBUNIT	Synthase
25283	3161	BETA-1,3-GLUCANASE	Glycosylase
25318	3162	TREHALOSE-6-PHOSPHATE PHOSPHATASE	Phosphatase
25326	3163	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
25352	3164	RECEPTOR-LIKE KINASE[PUTATIVE]	Kinase, Protein
25355	3165	LECTIN-LIKE PROTEIN KINASE[PUTATIVE]	Kinase, Protein
25357	3166	ANTHOCYANIDIN-3-GLUCOSIDE RHAMNOSYLTRANSFERASE	Transfases
25370	3167	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein

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25371	3168	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
25373	3169	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE-LIKE PROTEIN	Glycosylase
25383	3170	RECEPTOR PROTEIN KINASE-LIKE [PUTATIVE]	Kinase, Protein
25386	3171	ARGININE METHYLTRANSFERASE[PUTATIVE]	Transferases
25389	3172	URIDYLYL TRANSFERASES-LIKE	Transferases
25399	3173	AMINO ACID TRANSPORTER PROTEIN-LIKE	Transporter
25406	3174	PROLYL 4-HYDROXYLASE, ALPHA SUBUNIT-LIKE PROTEIN	Hydroxylase
25408	3175	PROTEIN PHOSPHATASE 2C-LIKE PROTEIN	Phosphatase
25412	3176	3-DEHYDROQUINATE SYNTHASE-LIKE PROTEIN	Synthase
25415	3177	ALPHA-MANNOSIDASE	Glycosylase
25419	3178	FERREDOXIN-NADP+ REDUCTASE	Reductase
25422	3179	CHALCONE ISOMERASE-LIKE PROTEIN	Isomerase
25433	3180	ELICITOR-INDUCIBLE RECEPTOR-LIKE PROTEIN[PUTATIVE]	Receptor
25439	3181	PEROXIDASE (EMB CAA66964.1)	Oxidase
25443	3182	S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN	Transferases
25446	3183	MANNAN ENDO-1,4-BETA-MANNOSIDASE	Glycosylase
25469	3184	UTP-GLUCOSE GLUCOSYLTRANSFERASE	Transferases
25479	3185	PROTEIN KINASE[PUTATIVE]	Kinase, Protein
25492	3186	PECTINESTERASE LIKE PROTEIN	Esterase
25503	3187	ZEAXANTHIN EPOXIDASE PRECURSOR	Oxidase
25509	3188	SUBTILISIN-TYPE PROTEASE-LIKE	Protease
25510	3189	DNA POLYMERASE ALPHA 1	Polymerase
25513	3190	MAP3K-LIKE PROTEIN KINASE[PUTATIVE]	Kinase, Protein
25515	3191	ANTHRANILATE N-TRANSFERASE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN	Transferases

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25516	3192	ANTHRANILATE HYDROXYCINNAMOYL/BENZOYLTRANSFERASE-LIKE PROTEIN	N-Transferases
25520	3193	RECEPTOR PROTEIN KINASE-LIKE PROTEIN	Kinase, Protein
25523	3194	UDP-GLUCURONYLTRANSFERASE-LIKE PROTEIN	Transferases
25528	3195	RECEPTOR-LIKE PROTEIN KINASE	Kinase, Protein
25536	3196	CUCUMISIN-LIKE SERINE PROTEASE (GB AAC18851.1)	Protease
25540	3197	PEROXIDASE (EMB CAA66967.1)	Oxidase
25543	3198	N-ACETYLTRANSFERASE HOOKLESS1-LIKE PROTEIN	Transferases
113old	3199	ACCELERATED CELL DEATH 2; RED CHLOROPHYLL CATABOLITE REDUCTASE [ARABIDOPSIS THALIANA]	Reductase
12old	3200	LETHAL LEAF-SPOT 1 HOMOLOG LLS1 [DIOXYGENASE DOMAIN][ARABIDOPSIS THALIANA].	Oxygenase
13288old	3201	(EC 4.2.99.8) CYSCI [SIMILARITY] - ARABIDOPSIS THALIANA.	
15402old	3202	CYSTEINE SYNTHASE (EC 4.2.99.8) 3A, CYTOSOLIC - ARABIDOPSIS THALIANA.	Synthase
15792old	3203	CYSTEINE SYNTHASE (EC 4.2.99.8) ISOFORM 5-8, CYTOSOLIC - ARABIDOPSIS THALIANA.	Synthase
15851old	3204	CYSTEINE SYNTHASE (EC 4.2.99.8) ACS1 - ARABIDOPSIS THALIANA.	Synthase
1678old	3205	CYSTEINE SYNTHASE; O-ACETYL SERINE(THIOL) LYASE [ARABIDOPSIS THALIANA].	Synthase
182old	3206	PROBABLE CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYL SERINE SULPHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE) (OAS-TL) (CS26).	Synthase
18927old	3207	PUTATIVE CYSTEINE SYNTHASE; 39489-37437 [ARABIDOPSIS THALIANA].	Synthase
203old	3208	5-METHYLtetrahydropteroyltriglutamate- HOMOCYSTEINE METHYLTRANSFERASE (VITAMIN- B12-INDEPENDENT METHIONINE SYNTHASE ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE ISOZYME).	Transferases

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21308old	3209	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
21309old	3210	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
23001old	3211	4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
23094old	3212	CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O- ACETYL SERINE-SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE).	Synthase
34209old	3213	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
34659old	3214	CYSTEINE SYNTHASE ATCYSCI [ARABIDOPSIS THALIANA].	Synthase
37280old	3215	CYSTEINE SYNTHASE, MITOCHONDRIAL PRECURSOR (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE).	Synthase
37284old	3216	CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE).	Synthase
39272old	3217	CHLOROPHYLL B SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
40108old	3218	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
40109old	3219	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
42762old	3220	5'-PHOSPHORIBOSYL-5-AMINOIMIDAZOLE SYNTHETASE.	Synthase
42911old	3221	PUTATIVE CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
44492old	3222	SIMILAR TO NICOTIANA 5-EPI-ARISTOLOCHENE SYNTHASE (GB)	Synthase
44907old	3223	CYSTEINE SYNTHASE (EC 4.2.99.8) 3A - ARABIDOPSIS THALIANA.	Synthase
44988old	3224	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
45432old	3225	CYSTEINE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase
46254old	3226	3-DEOXY-D-ARABINO-HEPTULOSONATE PHOSPHATE SYNTHASE.	7- Synthase
7417old	3227	2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE SYNTHASE [ARABIDOPSIS THALIANA].	Synthase

Many annotations in publicly accessible data bases occur repeatedly, i.e. for various nucleic acid or amino acid sequences. The reasons for this are, to a minor extent, erroneous and/or redundant sequences and descriptions. To a major extent, this reflects the fact that proteins with the same function do indeed occur repeatedly in
5 the genome. These different proteins can differ from each other for example by the regulation of their expression or by their cellular localization.

Many proteins belong to particular protein families. The skilled worker can draw conclusions with regard to the type of function, and thus also the possibility of an
10 assay method for the polypeptide in question or its biological activity, from the protein family it belongs to. A description of such families of polypeptides and genes from *Arabidopsis* is obtainable for example in EP-A-1 033 405, but can also be found in the literature with which the skilled worker is familiar. Corresponding related information regarding the individual targets in Table 1 can be found in the
15 document cited or in the general literature.

The analysis carried out for the purpose of the present invention, however, provides not only the general descriptions and the descriptions which are less suitable for the choice of herbicide targets in EP-A-1 033 405, but also the specificity of the
20 polypeptide for the plant kingdom and the groups enzyme, receptor or channel (transporter) and more specific classes of these groups to which the proteins belong. The method according to the invention thus makes it possible to identify the particular suitability of a protein as target for finding lead structures for new herbicides exclusively with the aid of the method according to the invention. The
25 classes which the polypeptides according to the invention were assigned to comprise, inter alia, acetylases, aldolases, amidases, amylases, anhydrases, arginases, ATPases, carboxylases, carrier-proteins, cellulases, channels, chelatases, chitinases, cyclases, deaminases, decarboxylases, dehydratases, dehydrogenases, desaturases, enolases,
30 epimerases, esterases, furanases, furanosidases, galactosidases, galacturonases, glucanases, glucosidases, glucosylases, glucuronases, glycosylases, GTPases,

helicases, hydrolases, hydroxylases, isomerases, kinases, LACCases, lactonases, ligases, lipases, lyases, mannosidases, maturases, methylases, mutases, nucleases, nucleosidases, nucleotidases, oxidases, oxygenases, pectases, pectosidases, peptidases, permeases, phosphatases, phosphorylases, polymerases, proteases, 5 racemases, receptors, reductases, sulfurylases, synthases, synthetases, transferases, transporters, transcriptases, xylanases and xylosidases.

The polypeptides which are identified by means of the method according to the invention are therefore particularly suitable as targets for finding new herbicidal 10 active compounds. They are particularly suitable because they

- a) have no homologous counterpart in animal organisms or in humans, according to the method according to the invention (determination of E-values, alignment of data bases),
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- b) were selected with a view that they are enzymes with small ligands or else receptors or channels which can, as a rule, be modulated, i.e. inhibited or activated, by small organic molecules or peptides and are therefore in principle open to being influenced by an active compound, and
20
- c) owing to the assignment to particular groups, make it possible for the skilled worker to select in a direct and obvious fashion assay methods which are suitable for the particular classes of polypeptides. To this end, the skilled worker can rely on the current literature or exploit the assay methods
25 described in the present application.

Subject-matter of the present invention is therefore furthermore the use of polypeptides found with the aid of the method according to the invention or of the nucleic acids encoding these polypeptides in methods for finding modulators of the 30 polypeptides according to the invention or for finding new herbicidal compounds.

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Subject-matter of the present invention is in particular the use of one of the polypeptides of SEQ ID NO: 1 to SEQ ID NO: 3227 in methods for finding modulators of these polypeptides or for finding new herbicidal compounds.

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The subject-matter of the present invention is furthermore the use of polypeptides which exert at least the biological activity of one of the polypeptides according to the invention and which encompass an amino acid sequence which has at least 60% identity, preferably 80% identity, especially preferably 90% identity, very especially 10 preferably 97% identity, with a sequence of SEQ ID NO: 1 to SEQ ID NO: 3227 over its entire length in methods for finding modulators of the polypeptides or for finding new herbicidal active compounds.

15 The degree of identity of the amino acid sequences is determined for example with the aid of the program BLASTP + BEAUTY Version 2.0 4. (Altschul et al., 1997).

Preferred polypeptides which are used in the methods for finding modulators of the polypeptides according to the invention are those of SEQ ID NO: 1 to SEQ ID NO: 3227.

20 Based on the genetic code, a nucleic acid sequence encoding these polypeptides can be deduced in a simple fashion from the amino acid sequences of the polypeptides according to the invention, which amino acid sequences are shown in the sequence listing.

25 Such deduced nucleic acids can be used as probes and/or primers for detection and/or isolation of related polynucleotide sequences in different organisms, preferably in plants, through hybridization. Depending on the stringency of the conditions under which these probes and primers are used, polynucleotides exhibiting a wide range of similarity to those shown in Table 1 can be detected or isolated. "Stringency" as used 30 herein is a function of probe length, probe composition (G/C content) and salt

concentration, organic solvent concentration and temperature of hybridization or wash conditions. Stringency is typically compared by the parameter T_m , which is the temperature of hybridization or wash conditions. Stringency is typically compared by the parameter T_m which is the temperature at which 50% of the complementary molecules in the hybridization are hybridized. High stringency conditions are e.g. those providing a condition of T_m 5°C to 10°C. Medium or moderate stringency conditions are those providing T_m 20°C to tm 29°C. Low stringency conditions are those providing for a condition of tm 40°C to T_m 48°C. The relationship of hybridization conditions to T_m (in °C) is expressed in the following equation:

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$$T_m = 81.5 - 16.6 (\log_{10}[\text{Na}^+] + 0.41(\%G+C)) - (600/N),$$

where N is the length of the probe. This equation works well for probes comprising 14 to 70 nucleotides in length that are identical to the target sequence.

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Subject-matter of the present invention is therefore also the use of the nucleic acids encoding the polypeptides according to the invention in methods for finding new herbicidal compounds, and of DNA constructs which encompass one of the deduced nucleic acid sequences and a homologous or heterologous promoter.

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The term "homologous promoter" as used in the present context refers to a promoter which controls the expression of the gene in question in the original organism.

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The term "heterologous promoter" as used in the present context refers to a promoter which has properties other than the promoter which controls the expression of the gene in question in the original organism.

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The choice of heterologous promoters depends on whether pro- or eukaryotic cells or cell-free systems are used for expression. Examples of heterologous promoters are the cauliflower mosaic virus 35S promoter for plant cells, the alcohol dehydrogenase

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promoter for yeast cells, the T3, T7 or SP6 promoters for prokaryotic cells or cell-free systems.

Subject-matter of the present invention is furthermore vectors comprising a nucleic acid encoding a polypeptide according to the invention or an abovementioned DNA construct. Vectors which can be used are all those phages, plasmids, phagemids, phasmides, cosmids, YACs, BACs, artificial chromosomes or particles which are suitable for particle bombardment, which are used in molecular biology laboratories.

Preferred vectors are pBIN (Bevan, 1984) and its derivatives for plant cells, pFL61 (Minet *et al.*, 1992) or, for example, the p4XXprom. vector series(Mumberg *et al.*) for yeast cells, pSPORT vectors (Life Technologies) for bacterial cells, lambdaZAP (Stratagene) for phages or Gateway vectors (Life Technologies) for various expression systems in bacterial cells or Baculovirus.

Subject-matter of the present invention is furthermore host cells comprising at least one nucleic acid encoding one of the polypeptides according to the invention or a DNA construct according to the invention or a vector according to the invention.

The term "host cell" as used in the present context refers to cells which do not naturally comprise the nucleic acids to be used in accordance with the invention.

Suitable host cells are prokaryotic cells, preferably *E. coli*, but also eukaryotic cells, such as cells of *Saccharomyces cerevisiae*, *Pichia pastoris*, insects, plants, frog oocytes and mammalian cell lines.

The term "polypeptides" as used in the present context refers not only to short amino acid chains which are usually termed peptides, oligopeptides or oligomers, but also to longer amino acid chains which are usually termed proteins. It encompasses amino acid chains which can be modified either by natural processes, such as post-

translational processing, or by chemical prior-art methods. Such modifications may occur at various sites and repeatedly in a polypeptide, such as, for example, on the peptide backbone, on the amino acid side chain, on the amino and/or the carboxyl terminal. For example, they encompass acetylations, acylations, ADP ribosylations, 5 amidations, covalent linkages to flavins, haeme moieties, nucleotides or nucleotide derivatives, lipids or lipid derivatives or phosphatidylinositol, cyclisation, disulfide bridge formations, demethylations, cystine formations, formylations, gamma-carboxylations, glycosylations, hydroxylations, iodinations, methylations, myristoylations, oxidations, proteolytic processings, phosphorylations, selenoylations 10 and tRNA-mediated amino acid additions.

The polypeptides to be used in accordance with the invention may exist in the form of "mature" proteins or as parts of larger proteins, for example as fusion proteins. They can furthermore exhibit secretion or leader sequences, pro-sequences, 15 sequences which make possible simple purification, such as polyhistidine residues, or additional stabilizing amino acids.

The polypeptides to be used in accordance with the invention need not constitute complete plant proteins but may also only be fragments thereof, as long as they retain 20 at least one biological activity of the complete plant proteins. Polypeptides which exert the same type of biological activity as one of the proteins of Table 1 are still considered as being within the scope of the present invention. In this context, it is not necessary for the polypeptides to be used in accordance with the invention to be deducible from *Arabidopsis* proteins. Polypeptides which correspond to proteins of, 25 for example, the plants given hereinbelow or fragments of these proteins which can still exert their biological activity are also considered as being within the scope of the present invention: tobacco, maize, wheat, barley, oats, oil seed rape, rice, rye, soya bean, tomatoes, legumes, potato plants, *Lactuca sativa*, Brassicae, woody species, *Physcomitrella patens*.

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In comparison with the corresponding regions of the naturally occurring polypeptides, the polypeptides according to the invention can have deletions or amino acid substitutions as long as they still exert at least one biological activity of the complete polypeptides. Conservative substitutions are preferred. Such 5 conservative substitutions encompass variations, one amino acid being replaced by another amino acid from among the following group:

1. Small aliphatic residues, unpolar residues or residues of little polarity: Ala, Ser, Thr, Pro and Gly;
- 10 2. Polar, negatively charged residues and their amides: Asp, Asn, Glu and Gln;
3. Polar, positively charged residues: His, Arg and Lys;
4. Large aliphatic unpolar residues: Met, Leu, Ile, Val and Cys; and
5. Aromatic residues: Phe, Tyr and Trp.

15 The following list shows preferred conservative substitutions:

Original residue	Substitution
Ala	Gly, Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Ala, Pro
His	Asn, Gln
Ile	Leu, Val, Met
Leu	Ile, Val, Met
Lys	Arg,
Met	Leu, Ile

Original residue	Substitution
Phe	Met, Leu, Tyr, Ile, Trp
Pro	Gly
Ser	Thr
Thr	Ser
Trp	Tyr, Phe
Tyr	Trp, Phe
Val	Ile, Leu

The skilled worker knows that the polypeptides of the present invention can be obtained by various routes, for example by chemical methods such as the solid-phase method. To obtain larger protein quantities, the use of recombinant methods is recommended. The expression of a cloned gene according to the invention or fragments thereof can be effected in a series of suitable host cells which are known to the skilled worker. To this end, a nucleic acid encoding one of the polypeptides according to the invention or a DNA construct according to the invention or vector is introduced into a host cell with the aid of known methods.

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The integration into the chromosome of the host cell, of the cloned nucleic acid according to the invention which is suitable for expressing the polypeptide according to the invention, is within the scope of the present invention. This nucleic acid or fragments thereof are preferably introduced into a plasmid, and the coding regions of the nucleic acids or fragments thereof are linked functionally to a constitutive or inducible promoter.

The basic steps for preparing the recombinant polypeptides according to the invention are :

20

1. Obtaining a natural, synthetic or semi-synthetic nucleic acid (DNA) which encodes a polypeptide according to the invention.

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2. Introducing this DNA into an expression vector which is suitable for expressing the polypeptide according to the invention, either alone or as a fusion protein.

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3. Transforming a suitable host cell, preferably a prokaryotic host cell, with this expression vector.

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4. Growing this transformed host cell in a manner which is suitable for expressing the polypeptide according to the invention.

15 5. Harvesting the cells and isolating the polypeptide according to the invention by suitable, known methods.

15 In this context, the coding regions of the polypeptide according to the invention can be expressed for example in *E. coli* using the customary methods. Suitable expression systems for *E. coli* are commercially available, for example the expression vectors of the pET series, such as pET3a, pET23a, pET28a with His-tag or pET32a with His-tag for simple purification and thioredoxin fusion for increasing the solubility of the expressed enzyme, and pGEX with glutathione synthetase fusion, and also the pSPORT vectors, with the possibility of transferring the coding region into different vectors of the Gateway system for various expression systems. The expression vectors are transformed into λ DE3-lysogenic *E. coli* strains, for example, BL21(DE3), HMS 174(DE3) or AD494(DE3). After the initial growth of the cells under standard conditions known to the skilled worker, expression is induced by means of IPTG. After induction of the cells, incubation is carried out for 3 to 24 hours at temperatures of from 18 to 37°C. The cells are disrupted by sonication in breaking buffer (10 to 200 mM sodium phosphate, 100 to 500 mM NaCl, pH 5 to 8. The protein expressed can be purified by chromatographic methods,

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in the case of protein expressed with His-tag by chromatography on an Ni-NTA column.

Another favourable approach is the expression of a polypeptide according to the invention in commercially available yeast strains (for example, *Pichia pastoris*) or in insect cell cultures (for example Sf9 cells).

Alternatively, the polypeptides according to the invention can also be expressed in plants.

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A rapid method of isolating the polypeptides according to the invention which are synthesized by host cells using a nucleic acid encoding them starts with the expression of a fusion protein, it being possible for the fusion moiety to be affinity-purified in a simple manner. The fusion moiety can be, for example, glutathione S-transferase. The fusion protein can then be purified on a glutathione affinity column. The fusion moiety can be cleaved off by partial proteolytic cleavage for example at linkers between the fusion moiety and the polypeptide according to the invention which is to be purified. The linker can be designed such that it includes target amino acids, such as arginine and lysine residues, which define sites for trypsin cleavage. In order to generate such linkers, standard cloning methods using oligonucleotides may be applied.

15

Other purification methods which are possible are based on preparative electrophoresis, FPLC, HPLC (for example using gel filtration columns, reverse-phase columns or mildly hydrophobic columns), gel filtration, differential precipitation, ion-exchange chromatography and affinity chromatography.

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The terms "isolation or purification" as used in the present context mean that the polypeptides according to the invention are separated from other proteins or other macromolecules of the cell or of the tissue. Preferably, a preparation comprising the

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polypeptides according to the invention is at least 10-fold concentrated and especially preferably at least 100-fold concentrated with regard to the protein content over a host cell preparation.

- 5 The polypeptides according to the invention can also be affinity-purified without fusion moieties with the aid of antibodies which bind to the polypeptides.

The polypeptides found here with the aid of the method according to the invention and the polypeptides which are homologous to them make possible the search for 10 new specific herbicides; thus, ways are opened up of identifying lead structures, some of which may be completely new, with the aid of these targets. Thus, new interesting herbicides can be provided starting from such compounds which inhibit the present polypeptides.

- 15 Not only the enzymes, receptors and channels stated, but other proteins with other functions, too, can be filtered out for their plant specificity. This also applies to proteins whose function is as yet unknown.

Just as described above for finding new targets for herbicides, fungus- or insect-specific targets can be identified. For this purpose, the genomes of relevant 20 phytopathogenic fungi, for example, *Magnaporthe* and many others, or insects, for example *Drosophila*, *Heliothis* and many others, are compared with the genomes of plants and animals. Thus, those enzymes, receptors and channels which are fungus-specific (and which do not occur in plants or animals) or which are insect-specific 25 (and which do not occur in plants or higher animals, that is to say Chordata, in particular humans), can be identified.

The search for lead structures by target-based screening has played a key role for approximately 10 years in the search for pharmaceutical active compounds. In crop protection research, the same key position has emerged somewhat later. Owing to 30

this high relevance, a multiplicity of methods have been developed for verifying any new target. Also included are methods of expressing the genes in relevant systems with which the skilled worker in the field of various families of proteins or classes of enzymes is generally familiar.

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Enzymes and how they are affected by active compound candidate molecules can be measured quite generally on the basis of their enzymatic activity. The enzymatic conversion of starting materials to products can be determined in a multiplicity of ways: for example by monitoring the optical characteristics of the reaction solution 10 (for example absorption, fluorescence, luminescence). If the enzymatic reaction cannot be monitored visually directly, the reaction can frequently be monitored by coupling with one or more further reactions, either enzymatic or non-enzymatic reactions, which can be monitored visually. As an alternative, a multiplicity of variants of binding assays have been developed which are based on measuring the 15 binding of active compound candidate molecules to a protein. Binding assays can be carried out using radiolabeled or optically labeled detection molecules. Binding assays can also be carried out without labels, for example by methods of mass spectrometry or nuclear resonance spectrometry. This is in sharp contrast to the protein functions, which can be tested by cellular assays. Here, cells are constructed 20 in a variety of ways which respond in a specific manner to the inhibition (or activation) of an enzyme (or receptor or channel). For example, bacteria can be constructed whose intrinsic enzyme has been switched off and was then replaced by a corresponding plant enzyme. When the action of active compound candidate molecules on the wild-type bacterial strain and the transgenic strain are compared, 25 active compounds can be identified which relate to the plant enzyme. Cellular assays can preferably be used for assaying in particular receptors, but also channels. For example, non-plant cells can be constructed which recombinantly comprise a plant receptor and which visualize the response of the receptor to active compound candidate molecules visually. Thus, a luciferase can be expressed in receptor-mediated fashion, for example, and this luciferase can then be detected with high 30

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sensitivity. Channels which are ion-selective, in particular for calcium, can be detected for example by ion-selective stains.

The multiplicity of possibilities of opening up enzymes, receptors and channels to screening, preferably HTS or UHTS, is described in various reviews (see, for example, J. A. Landro et al., *J. Pharmacol. Toxicol. Methods* 44 (2201) 273 - 289). A large number of public fora exist for the specialists working in this field, such as, for example, the "Society for Biomolecular Screening" (Danbury, CT, USA) (www.sbsonline.org), which publishes its own periodical. The annual conferences of the "Society for Biomolecular Screening" reflect the current state of the art. It can therefore be said that it is currently possible to convert any desired protein into an HTS assay, it being possible for the difficulty or complexity of the assay method to vary, depending on the polypeptide.

Many assay systems whose aim it is to assay compounds and natural extracts are designed for high throughput numbers in order to maximize the number of substances studied within a given period. Assay systems which are based on cell-free procedures require purified or semipurified protein. They are suitable for a "first" assay, whose principal aim is to detect a potential effect of a substance on the target protein.

Effects such as cell toxicity are, as a rule, ignored in these *in vitro* systems. The assay systems test both inhibitory or suppressive effects of the substances and stimulatory effects. The efficacy of a substance can be tested by concentration-dependent test series. Control batches without test substances can be used for assessing the effects.

In the following text, methods shall be shown by way of example which can be exploited inter alia for finding modulators of the polypeptides according to the invention, the methods according to the invention including high-throughput screening (HTS) and ultra-high throughput screening (UHTS). Both host cells and

cell-free preparations comprising the nucleic acids according to the invention and/or the polypeptides according to the invention can be used for this purpose.

5 The examples given are understood as being a nonlimiting selection of methods which are possible for use for the purpose in accordance with the invention.

Activity assays

In order to find modulators of the polypeptides to be used according to the invention, for example a synthetic reaction mix (for example products of the *in vitro* transcription) or a cellular component, such as a crude cell extract, or any other preparation comprising the polypeptide to be used in accordance with the invention can be incubated together with one or more optionally labeled substrates or ligands of the polypeptides in the presence or absence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule of increasing or 10 inhibiting the activity of the polypeptide to be used in accordance with the invention can be seen from an increased or reduced conversion of the substrate. Molecules which lead to an increased activity of the polypeptides to be used in accordance with the invention are agonists. Molecules which lead to a reduction in the activity of the polypeptides to be used in accordance with the invention are probably inhibitors or 15 antagonists. The detection of the biological activity of the polypeptides to be used in accordance with the invention can possibly be improved by what is known as a reporter system. Reporter systems as used herein comprise, but are not limited to, colorimetrically labeled substrates which are converted into a product, or a reporter gene which responds to changes in the activity or the expression of the polypeptides 20 to be used in accordance with the invention.

Binding assays

In order to find modulators of the polypeptides to be used according to the invention, for example a synthetic reaction mix (for example products of the *in vitro* transcription) or a cellular component, such as a crude cell extract, or any other 30

preparation comprising the polypeptide to be used in accordance with the invention can be incubated together with a labeled substrate or ligand of the polypeptides in the presence or absence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule of increasing or inhibiting the activity of the 5 polypeptide to be used in accordance with the invention can be seen from an increased or reduced binding of the labeled ligand. Molecules which bind well and lead to an increased activity of the polypeptides to be used in accordance with the invention are agonists. Molecules which bind well but do not trigger the biological activity of the polypeptides to be used in accordance with the invention are probably 10 good antagonists. The detection of the biological activity of the polypeptides to be used in accordance with the invention can possibly be improved by what is known as a reporter system. Reporter systems as used herein comprise, but are not limited to, a reporter gene which responds to changes in the activity or expression of the polypeptides to be used in accordance with the invention, or other known binding 15 assays.

Displacement assays

A further example of a method by means of which modulators of the polypeptides to be used in accordance with the invention can be found is a displacement assay in 20 which the polypeptides to be used in accordance with the invention and a potential modulator are contacted under suitable conditions with a molecule which is known to bind to the polypeptides to be used in accordance with the invention, such as a natural substrate or ligand, or a substrate or ligand mimetic. The polypeptides to be used in accordance with the invention can be labeled themselves, for example 25 radiolabeled or colorimetrically labeled, so that the number of the polypeptides which are bound to a ligand or which have undergone a conversion can be determined accurately. In this manner, the efficacy of an agonist or antagonist can be determined.

For the purposes of molecular interaction studies using a polypeptide according to the invention, or else with polypeptide variants which have been modified by *in vitro* mutagenesis or other known methods, a known analytical system may be employed, for example by Biacore AB, Uppsala, Sweden. In this system, (i) the polypeptide according to the invention or fragments thereof can be coupled to a biochip via known chemical methods (coupling via amines, thiols, aldehydes) or affinity binding (for example Streptavidin-Biotin, IMAC), or (ii) a ligand, for example a peptide or a small molecule, can be coupled to the chip. The binding, to the immobilized molecules, of a ligand in solution can be measured physically. In the case of the Biacore Instrument, the ligand is immobilized on a sensor chip with a thin gold layer. The solution of the analyte is perfused through a micro-flow cell on the chip. The binding of the analyte to the immobilized ligand increases the local concentration at the surface, the refractive index of the medium close to the gold layer gradually increasing. This affects the interaction between free electrons (plasmons) in the metal and photons which are emitted by the instrument. These physical changes are proportional to the mass and molecular number on the chip, the ligand-analyte binding is registered in real time, thus allowing the apparent association/dissociation rate to be determined (Fivash et al. 1998). Competition experiments validate the specificity of the binding. Analogous measurements also serve to determine the polypeptide domains which are important for the binding of ligands, and to identify new, as yet unknown, ligands of the polypeptides according to the invention.

Scintillation Proximity Assay (SPA)

A possibility of identifying substances which modulate the activity of specific polypeptides according to the invention, such as, for example, receptor proteins, and polypeptides which are homologous thereto, is what is known as "Scintillation Proximity Assay" (SPA), see EP 015 473. This assay system exploits the interaction of a receptor with a radiolabeled ligand (for example a small organic molecule or a second radiolabeled protein molecule). The receptor is bound to microspheres or beads provided with scintillating molecules. As the radioactivity declines, the

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scintillating substance in the microsphere is excited by the subatomic particles of the radiolabel, and a detectable photon is emitted. The assay conditions are optimized in such a way that only those particles originating from the ligand lead to a signal which originate from a ligand bound to the receptor or to the polypeptide according to the
5 invention.

In a possible embodiment, the polypeptide according to the invention is bound to the beads, either together with, or without, interacting or binding test substances. It would also be possible to use fragments of the polypeptides according to the
10 invention. When a binding, for example radiolabeled, ligand binds to the immobilized polypeptide according to the invention, this ligand should inhibit or cancel out an existing interaction between the immobilized polypeptide according to the invention and the labeled ligand in order to bind itself in the contact area zone. Successful binding to the polypeptide according to the invention can then be detected
15 by means of a flash of light. Analogously, an existing complex between an immobilized polypeptide and a free, labeled ligand is destroyed by the binding of a test substance, which leads to a drop in the intensity of the flash of light which is detected. In this case, the assay system corresponds to a complementary inhibition system.
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Two Hybrid System

An example of an assay system based on intact cells is what is known as the Two Hybrid System, which is particularly suitable for those polypeptides which have a suitable interaction partner in the cell - a further polypeptide or peptide. A specific
25 example is what is known as the interaction trap. This is a genetic selection of interacting proteins in yeast (see, for example, Gyuris et al. 1993). The assay system is designed to detect and describe the interaction of two proteins, owing to an interaction which has taken place leading to a detectable signal.

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Such an assay system can also be adapted to the testing of large numbers of test substances in a given period.

The system is based on the construction of two vectors, the bait vector and the prey vector. A gene encoding a polypeptide according to the invention or fragments thereof is cloned into the bait vector and then expressed as fusion protein together with the LexA protein, a DNA binding protein. A second gene encoding an interaction partner of the polypeptide in question is cloned into the prey vector, where it is expressed as fusion protein together with the B42 prey protein. Both vectors are present in a *Saccharomyces cerevisiae* host which contains copies of LexA-binding DNA 5' of a lacZ or HIS3 reporter gene. If an interaction takes place between the two fusion proteins, activation of the transcription of the reporter gene results. If the presence of a test substance results in inhibition or interference with the interaction, the two fusion proteins can no longer interact and the product of the reporter gene is no longer produced.

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Calcium Imaging

5 Calcium imaging or signalling must be considered as a further method of detecting substances which interact with polypeptides according to the invention. This method is suitable, for example, for receptors which act as Ca^{2+} channels. Here, calcium indicators are employed with the aid of which changes in the intracellular calcium level are made detectable. Within the scope of these methods, cells which express the relevant polypeptide according to the invention are employed, and these cells are loaded with calcium indicators. Upon UV excitation, an influx of calcium caused by 10 an HC110-R agonist, or the release of intracellular calcium, leads to a change in absorption as a function of the calcium load of the indicator. In such a system, an antagonist can be recognized by the complete or partial suppression of the calcium signal induced by the agonist (for example α -LTX). Suitable calcium indicators which are possible for this purpose are Fura-2 (Sigma) or Indo-1 (Molecular Probes).

15 Further calcium indicators can be excited by visible light and change their fluorescence behaviour detectably as a function of their calcium load. The indicators Fluo-3 and Fluo-4 show high affinity for calcium. Fluo-4, which has the stronger fluorescence signal, is particularly suitable for measurements in test systems where 20 the cells are employed only at low density, as is the case for HEK293 cells. Further indicators are Rhod-2, x-Rhod-1, Fluo-5N, Fluo-5F, Mag-Fluo-4, Rhod-5F, Rhod-5N, Y-Rhod-5N, Mag-Rhod-2, Mag-X-Rhod-1, Calcium Green-1 and -2, Calcium Green-5N, Oregon Green 488 BAPTA-1, Oregon Green 488 BAPTA-2 and -5N, Fura Red, Calcein and the like.

25 An alternative to loading cells with calcium indicators is the recombinant expression of photoproteins in the target cells. Once these photoproteins have formed a complex with calcium ions, they react in the form of a light emission. A photoprotein which has already been used often in a large number of studies and assay systems is 30 aequorin. In this assay method, the cells which simultaneously express the target

protein and the aequorin are first loaded with the luminophore coelenterazin. The apoaequorin formed by the cells forms a complex with the coelenterazin and carbon dioxide. If calcium subsequently enters the cell and binds to the complex, carbon dioxide and blue light are emitted (emission maximum ~466 nm). The light emission 5 correlates with the calcium concentration which prevails intracellularly.

Subject-matter of the present invention is therefore in particular also the use of the polypeptides of the Table 1 which have been identified with the aid of the present method in methods of finding modulators of the polypeptides according to the 10 invention.

Subject-matter of the present invention is furthermore the use of nucleic acids encoding these plant proteins, DNA constructs comprising them, host cells comprising them, or antibodies which bind to these proteins in methods of finding 15 modulators of the polypeptides according to the invention.

The term "agonist" as used in the present context refers to a molecule which accelerates or increases the activity of the protein.

20 The term "antagonist" as used in the present context refers to a molecule which slows down or prevents the activity of the protein.

25 The term "modulator" as used in the present context constitutes the generic term for agonist and antagonist. Modulators can be small organochemical molecules, peptides or antibodies which bind to the polypeptides to be used in accordance with the invention. Furthermore, modulators can be small organochemical molecules, peptides or antibodies which bind to a molecule which, in turn, binds to the polypeptides to be used in accordance with the invention, thus influencing their biological activity. Modulators can constitute natural substrates and ligands or of

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structural or functional mimetics thereof. However, the term "modulator" does not extend to the natural substrates and to ATP.

The modulators are preferably small organochemical compounds.

5

The binding of the modulators to the proteins to be used in accordance with the invention can modify the cellular processes in such a way which lead to the death of the plants treated therewith.

10

Subject-matter of the present invention are therefore also modulators which have been found with the aid of one of the polypeptides described in accordance with SEQ ID NO:1 to SEQ ID NO:3227 for identifying modulators of a polypeptide.

15

Subject-matter of the invention is furthermore the use of modulators of the polypeptides in accordance with SEQ ID NO:1 to SEQ ID NO:3227 as herbicides.

20

Furthermore, the present invention comprises methods of finding chemical compounds which modify the expression of the polypeptides to be used in accordance with the invention. Such "expression modulators", again, can constitute growth-regulatory or herbicidal active compounds. Expression modulators can be small organochemical molecules, peptides or antibodies which bind to the regulatory regions of the nucleic acids encoding the polypeptides which are to be used in accordance with the invention. Furthermore, expression modulators can be small organochemical molecules, peptides or antibodies which bind to a molecule which, in turn, binds to regulatory regions of the nucleic acids encoding the polypeptides to be used in accordance with the invention, thus influencing their expression. Expression modulators can also be antisense molecules.

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The present invention therefore also extends to the use of modulators of the polypeptides according to the invention or of expression modulators of same as plant growth regulators or herbicides.

5 Subject-matter of the present invention are also expression modulators of proteins which are found with the aid of any above-described method of identifying expression modulators of the proteins.

10 Subject-matter of the invention is also the use of expression modulators as herbicides.

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Patent Claims

1. Method of identifying target proteins for herbicidally active compounds, comprising the following steps:
 - 5 a) alignment of a nucleic acid sequence or amino acid sequence (Group 1 sequence) from plants with a nucleic acid sequence or amino acid sequence from non-plant organisms (group 2 sequence) using suitable search parameters,
 - 10 b) determination of the E-value of the group 1 sequence and a similar group 2 sequence, and
 - 15 c) selecting group 1 sequences in which the exponent of the E-value exceeds that of the most similar group 2 sequence at least by a factor of 3.
2. Method according to Claim 1, characterized in that, in a further step, those group 1 sequences are selected which are essential for the plant and, if appropriate, naturally have small ligands.
 - 20 3. Method according to Claim 1 or 2, characterized in that the E-value is not lower than 10^{-30} .
 - 25 4. Use of polypeptides or of nucleic acids encoding them which are found in a method according to one of Claims 1 to 3 in a method of identifying modulators of these polypeptides or nucleic acids.

5. Use of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 and of the nucleic acids encoding them in methods of identifying modulators of these polypeptides.
- 5 6. Method of finding a chemical compound which modulates the activity of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
 - (a) contacting a preparation or host cell comprising the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and
 - 10 (b) identifying the chemical compound which specifically influences the activity of the polypeptide.
- 15 7. Method of finding a chemical compound which binds to one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 and/or which displaces a natural substrate or a natural ligand, comprising the following steps:
 - (a) contacting a preparation or host cell comprising the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of a chemical compound with the polypeptide, and
 - 20 (b) identifying the chemical compound which specifically binds to the polypeptide, and/or
- 25

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- (c) identifying the chemical compound which specifically displaces a natural substrate or a natural ligand.
8. Method of finding a chemical compound which modulates the cellular function of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
- (a) contacting a host cell which expresses the polypeptide with a chemical compound or a mixture of chemical compounds under conditions which permit the interaction of the chemical compound with the cell and/or the polypeptide, and
- (b) identifying the chemical compound which specifically influences the cellular function of the polypeptide.
- 15 9. Method of finding a compound which modifies the expression of the polypeptide in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227, comprising the following steps:
- (a) contacting a host cell expressing the polypeptide with a chemical compound or a mixture of chemical compounds,
- (b) determining the polypeptide concentration, and
- 25 (c) identifying the compound which specifically influences the expression of the polypeptide.
10. Use of a modulator of one of the polypeptides in accordance with SEQ ID NO: 1 to SEQ ID NO: 3227 as herbicide.

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11. Herbicides which are found in a method according to Claim 6 or 7.

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Declarations under Rule 4.17:

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(54) Title: POLYPEPTIDES FOR IDENTIFYING HERBICIDALLY ACTIVE COMPOUNDS

(57) Abstract: The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding herbicides, to the use of the polypeptides identified for identifying new, herbicidally active compounds, and methods of finding modulators of these polypeptides. Likewise, the invention relates to the use of the polypeptides in assay methods for identifying herbicidally active compounds.

INTERNATIONAL SEARCH REPORT

Internat. Application No
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IPC' 7 C07K14/415 C12N15/10 C12Q1/68 G01N33/50

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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00 58457 A (DIMSTER DENK DAGO F ; ROSETTA INPHARMATICS INC (US)) 5 October 2000 (2000-10-05) page 2, line 18 -page 5, line 17 page 14, line 14 - line 18 page 20, line 23 -page 21, line 31 page 37, line 12 -page 38, line 20 claims 11-20 ----	1-3 -/-

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE CABAB 'Online! AN 2000:34403, 1999 BERG D. ET AL: XP002197220 abstract & BERG D. ET AL.: "From genes to targets: impact of functional genomics on herbicide discovery" 1999 BRIGHTON CROP PROTECTION CONFERENCE: WEEDS. PROCEEDINGS OF AN INTERNATIONAL CONFERENCE, BRIGHTON, UK, 15-18 NOVEMBER 1999, (1999) NO. VOLUME 2, PP. 491-500. 11 REF. PUBLISHER: BRITISH CROP PROTECTION COUNCIL. FARNHAM MEETING INFO.: 1999 BRIGHTON, 1999,</p> <p>---</p>	
A	<p>ARIGONI ET AL: "A GENOME-BASED APPROACH FOR THE IDENTIFICATION OF ESSENTIAL BACTERIAL GENES" NATURE BIOTECHNOLOGY, NATURE PUBLISHING, US, vol. 16, no. 9, September 1998 (1998-09), pages 851-856, XP002119419 ISSN: 1087-0156 the whole document</p> <p>---</p>	
A	<p>WO 00 46405 A (PALSSON BERNHARD) 10 August 2000 (2000-08-10) page 4 -page 5</p> <p>---</p>	
A	<p>WO 01 44277 A (SYNGENTA PARTICIPATIONS AG ;BUDZISZEWSKI GREGORY JOSEPH (US); ZHOU) 21 June 2001 (2001-06-21) the whole document</p> <p>---</p>	
A	<p>WO 98 37206 A (HERSHEY HOWARD PAUL ;DU PONT (US); ABELL LYNN MARIE (US)) 27 August 1998 (1998-08-27) the whole document</p> <p>---</p>	
A	<p>WO 00 77185 A (NOVARTIS ERFIND VERWALT GMBH ;NOVARTIS AG (CH); BAUER MICHAEL WILL) 21 December 2000 (2000-12-21) the whole document</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

Int'l application No.
PCT/EP 01/09892

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: 4 because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-4

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-4

Method of identifying target proteins for herbicidally active compounds by alignment of plant derived sequences with sequences from other organisms, determination of the E-value, selecting sequences in which the exponent of the E-value of plant sequences exceeds that of the most similar sequence of a different organism by a factor of 3. Further, selecting plant essential sequences, especially those that have an E-value not less than 10(-30).

2. Claims: 5-11

Use of a polypeptide of SEQ ID NO:1-3227 and the nucleic acid encoding it in methods of identifying modulators of this polypeptide. Methods of finding chemical compounds which modulate the activity, bind to, displace a natural substrate or ligand of, modulate the cellular function, or modify the expression of the polypeptide.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 4

Present claim 4 relates to an extremely large number of possible compounds. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for none of the compounds claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, no search has been carried out.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Internat Application No
PCT/EP 01/09892

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 0058457	A 05-10-2000	AU 4186600 A US 2002103154 A		16-10-2000 01-08-2002
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WO 0077185	A 21-12-2000	AU 5532700 A EP 1185633 A		02-01-2001 13-03-2002

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